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OM protein - protein search, using sw model

Run on: February 19, 2004, 19:49:48 ; Search time 39 Seconds
(without alignments)
4321.865 Million cell updates/sec

Title: US-09-163-648-2
Perfect score: 4291
Sequence: 1 MSSSSWLLSLVAVTAQAQT.....ISKGNPGFQNTDDVQTSF 805

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues
Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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 - 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4291	100.0	805	10	US-09-978-385-2
2	4291	100.0	805	12	US-10-158-825-142
3	4291	100.0	805	15	US-10-158-847-142
4	4291	100.0	805	15	US-10-005-956-570
5	4291	100.0	805	15	US-10-005-956-843
6	4287	99.9	805	14	US-10-114-893-86
7	3775	88.0	711	10	US-09-969-384-13
8	3775	88.0	711	12	US-10-158-825-138
9	3775	88.0	711	15	US-10-158-847-138
10	3643	84.9	681	10	US-09-969-384-25
11	3643	84.9	681	12	US-10-158-825-140
12	3643	84.9	681	15	US-10-158-847-140
13	3579	83.4	805	10	US-09-978-385-6
14	3561	83.0	805	10	US-09-978-385-9
15	2979	69.4	555	12	US-10-137-870-72

16	2979	69.4	555	12	US-10-140-018-72	Sequence 72, Appl
17	2979	69.4	555	12	US-10-140-021-72	Sequence 72, Appl
18	2979	69.4	555	12	US-10-140-274-72	Sequence 72, Appl
19	2979	69.4	555	12	US-10-140-471-72	Sequence 72, Appl
20	2979	69.4	555	12	US-10-140-807-72	Sequence 72, Appl
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22	2979	69.4	555	12	US-10-140-924-72	Sequence 72, Appl
23	2979	69.4	555	12	US-10-140-926-72	Sequence 72, Appl
24	2979	69.4	555	12	US-10-141-698-72	Sequence 72, Appl
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39	2979	69.4	555	12	US-10-145-876-72	Sequence 72, Appl
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42	2979	69.4	555	12	US-10-146-725-72	Sequence 72, Appl
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44	2979	69.4	555	12	US-10-147-495-72	Sequence 72, Appl
45	2979	69.4	555	12	US-10-147-495-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-09-978-385-2
; Sequence 2, Application US/09978385
; Patent No. US20020177211A1
; GENERAL INFORMATION:
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Petrie, Charles
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME
; FILE REFERENCE: 99-24C1
; CURRENT APPLICATION NUMBER: US/09/978,385
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/133,952
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/151,181
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 09/563,516
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 805
; TYPE: PRI
; ORGANISM: Homo sapiens
US-09-978-385-2

Query Match 100.0%; Score 4291; DB 10; Length 805;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 NTMTIYSTGKVCNPNPQECCLLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180
QY 181 EYVVLKNEMARANHYEDYDGYWGDYEVNGVDYDYSRGOLIEDVHTTEEEKPLYEHL 240
DB 181 EYVVLKNEMARANHYEDYDGYWGDYEVNGVDYDYSRGOLIEDVHTTEEEKPLYEHL 240
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DB 241 HAYVRALMNAYPSPISPIGCLPAHLLGDMWGRFWTNLSYLVTFPGKPNIDVTDAMVDQ 300
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DB 301 AWDQRIIFKEAEKFFVSVGLPNNTOGFWENSMITDPGNVQKAVCHPTAWDLGKGFRLM 360
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DB 361 CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
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DB 481 KREIVGVVPEVPHDETYCDPASLFHVSNDYSFIRYRTLYQFOQEAALCOAAKHEGPHL 540
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DB 661 QMILFGEEDVRVANLKPRIISFNFFVTAPKNVSDIIPRTEVEKAIIRMSRINDAFRLND 720
QY 721 SLEFLGIQTLGPPNPPVSIWLVFGVVMGVIVGVILIFTGIRDRKKKKNKARSGENP 780
DB 721 SLEFLGIQTLGPPNPPVSIWLVFGVVMGVIVGVILIFTGIRDRKKKKNKARSGENP 780
QY 781 YASIDISKGNNPFGQNTDDVQTSF 805
DB 781 YASIDISKGNNPFGQNTDDVQTSF 805

RESULT 2
US-10-158-825-142
; Sequence 142, Application US/10158825
; Publication No. US20030138894A1
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF555
; CURRENT APPLICATION NUMBER: US/10/158,825
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/294,976
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 805
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-825-142

Query Match 100.0%; Score 4291; DB 12; Length 805;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 NNNAGDKWSAFLKEQSTLAQWYPLQEIQNTLVKLQALQOQSSSVLSSEKSKRLNTIL 120
DB 61 NNNAGDKWSAFLKEQSTLAQWYPLQEIQNTLVKLQALQOQSSSVLSSEKSKRLNTIL 120
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DB 181 EYVVLKNEMARANHYEDYDGYWGDYEVNGVDYDYSRGOLIEDVHTTEEEKPLYEHL 240
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DB 241 HAYVRALMNAYPSPISPIGCLPAHLLGDMWGRFWTNLSYLVTFPGKPNIDVTDAMVDQ 300
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QY 361 CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
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QY 421 IGLSPDFOEDNETEINFLLKQALTIIVGTLPTTYMLEKRWMMVFKGEIPKQOMKKWEM 480
DB 421 IGLSPDFOEDNETEINFLLKQALTIIVGTLPTTYMLEKRWMMVFKGEIPKQOMKKWEM 480
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QY 541 KCDISNSTEAGOKLFNMLRGKSEBWTALENVVGAKNMVRPLNLYFEPLFTWLKDQNK 600
DB 541 KCDISNSTEAGOKLFNMLRGKSEBWTALENVVGAKNMVRPLNLYFEPLFTWLKDQNK 600
QY 601 NSFVGNSTWSPYADQSIKVRISLSKALGDKAYEWNNDNEMYLFRSSVAYAMQYFLVKVN 660
DB 601 NSFVGNSTWSPYADQSIKVRISLSKALGDKAYEWNNDNEMYLFRSSVAYAMQYFLVKVN 660
QY 661 QMILFGEEDVRVANLKPRIISFNFFVTAPKNVSDIIPRTEVEKAIIRMSRINDAFRLND 720
DB 661 QMILFGEEDVRVANLKPRIISFNFFVTAPKNVSDIIPRTEVEKAIIRMSRINDAFRLND 720
QY 721 SLEFLGIQTLGPPNPPVSIWLVFGVVMGVIVGVILIFTGIRDRKKKKNKARSGENP 780
DB 721 SLEFLGIQTLGPPNPPVSIWLVFGVVMGVIVGVILIFTGIRDRKKKKNKARSGENP 780
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DB 781 YASIDISKGNNPFGQNTDDVQTSF 805

RESULT 3
US-10-158-847-142
; Sequence 142, Application US/10158847
; Publication No. US20030091557A1
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142

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; LENGTH: 805
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-847-142

Query Match      100.0%; Score 4291; DB 15; Length 805;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 NNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQALQONGSSVLSSEKSKRLNTIL 120

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Db 121 NTMSTIYSTGKVCNPNPQECCLLEPGLNEIMANSLDYNERNLWAWESWSEVKGQLRPLY 180

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Db 181 EBYVVLKNEMARANHVEDYDGYWRGDYEVNGVDGYDSRGQLIEDVEHTFEEIKPLYEHL 240

Qy 241 HAYVRAKLMNAYPSYISPIGCLPAHLGDMWGRFWTNLYSLTVPGQKPNIDVTDAMVDQ 300
Db 241 HAYVRAKLMNAYPSYISPIGCLPAHLGDMWGRFWTNLYSLTVPGQKPNIDVTDAMVDQ 300

Qy 301 AWAQRIKFEAEKFFVSVGLPNNTOGFWNSMLTDPGNVQKAVCHPTAWDLKGDFRILM 360
Db 301 AWAQRIKFEAEKFFVSVGLPNNTOGFWNSMLTDPGNVQKAVCHPTAWDLKGDFRILM 360

Qy 361 CTKVMTDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
Db 361 CTKVMTDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420

Qy 421 IGLLSPDFQEDNETEINFLLKQALITVGLTPFTYMLEKRWVFKGEIPKQWKKWEM 480
Db 421 IGLLSPDFQEDNETEINFLLKQALITVGLTPFTYMLEKRWVFKGEIPKQWKKWEM 480

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Db 481 KREIVGVVEVPDHDTEYCDPASLFHVSNDYSFIRYVYTRTLVQFQOEALCOAAKHEGPLH 540

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Db 781 YASIDISKGNPNPGONTDDVQTSF 805

RESULT 4
US-10-005-956-570
; Sequence 570, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
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QY 781 YASIDISKGNPPGONTDDVOTSF 805
Db 781 YASIDISKGNPPGONTDDVOTSF 805

RESULT 5
US-10-005-956-843
; Sequence 843, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 843
; LENGTH: 805
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-005-956-843

Query Match 100.0%; Score 4291; DB 15; Length 805;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFDLKFNHEADLFYQSSLASWNTNITEENVQ 60

QY 61 NNNAGDKWSAFLEKEOSTLAQMYPLQEIQLNLTVKLQALQNGSSVLSSEKSKRLNTIL 120
Db 61 NNNAGDKWSAFLEKEOSTLAQMYPLQEIQLNLTVKLQALQNGSSVLSSEKSKRLNTIL 120

QY 121 NTMSTIYSTGKVCNPNPQECLELLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180
Db 121 NTMSTIYSTGKVCNPNPQECLELLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180

QY 181 EYVVLKNEARANHEDYDGRGDEYVNGVDYDYSRGQLIEDVEHTFEIEKPLYEHL 240
Db 181 EYVVLKNEARANHEDYDGRGDEYVNGVDYDYSRGQLIEDVEHTFEIEKPLYEHL 240

QY 241 HAYVRKLMNAYPSYISPIGCLPAHLGDMWGRFNTNLSLTVPFGOKNIDVTAMVDQ 300
Db 241 HAYVRKLMNAYPSYISPIGCLPAHLGDMWGRFNTNLSLTVPFGOKNIDVTAMVDQ 300

QY 301 AWAQRIEKEAEKFFVSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAMDGLKGFRIIM 360
Db 301 AWAQRIEKEAEKFFVSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAMDGLKGFRIIM 360

QY 361 CTKVTDMPDLTAHEMGHIQYDWAYAAQPFLLRNGANEGFHAIVGIMSLSAATPKHLKS 420
Db 361 CTKVTDMPDLTAHEMGHIQYDWAYAAQPFLLRNGANEGFHAIVGIMSLSAATPKHLKS 420

QY 421 IGLSPDFQEDNETEINFLIKQALTIIVGTLPTFTMLKRWVWVFKGEIIPKDWKMKWEM 480
Db 421 IGLSPDFQEDNETEINFLIKQALTIIVGTLPTFTMLKRWVWVFKGEIIPKDWKMKWEM 480

QY 481 KREIVGVVEVPVPHDETCDPASLFHVSNDYSFIRYVTRTLYQFQOEALCOAAKHEGPHL 540
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QY 541 KDISNSTEAGOKLFNMLRIGKSEPTWLALENVVGAKMNVRLPLNFFPLFTWLKDQNK 600
Db 541 KDISNSTEAGOKLFNMLRIGKSEPTWLALENVVGAKMNVRLPLNFFPLFTWLKDQNK 600

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Db 661 QMILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLNDN 720

QY 721 SLEFLGIQPTLGPFPNPQPPVSIWLVGVVGMVIVVIGVILIFTGIRDRKKKKKARSGENP 780
Db 721 SLEFLGIQPTLGPFPNPQPPVSIWLVGVVGMVIVVIGVILIFTGIRDRKKKKKARSGENP 780

QY 781 YASIDISKGNPPGONTDDVOTSF 805
Db 781 YASIDISKGNPPGONTDDVOTSF 805

RESULT 6
US-10-114-893-86
; Sequence 86, Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Carlin-Duckett, McKeough
; APPLICANT: Kelleher, Kerry S.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6000-10A
; CURRENT APPLICATION NUMBER: US/10/114,893
; CURRENT FILING DATE: 2002-04-02
; EARLIER APPLICATION NUMBER: 09/413,232
; EARLIER FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-893-86

Query Match 99.9%; Score 4287; DB 14; Length 805;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 804; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFDLKFNHEADLFYQSSLASWNTNITEENVQ 60
Db 1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFDLKFNHEADLFYQSSLASWNTNITEENVQ 60

QY 61 NNNAGDKWSAFLEKEOSTLAQMYPLQEIQLNLTVKLQALQNGSSVLSSEKSKRLNTIL 120
Db 61 NNNAGDKWSAFLEKEOSTLAQMYPLQEIQLNLTVKLQALQNGSSVLSSEKSKRLNTIL 120

QY 121 NTMSTIYSTGKVCNPNPQECLELLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180
Db 121 NTMSTIYSTGKVCNPNPQECLELLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180

QY 181 EYVVLKNEARANHEDYDGRGDEYVNGVDYDYSRGQLIEDVEHTFEIEKPLYEHL 240
Db 181 EYVVLKNEARANHEDYDGRGDEYVNGVDYDYSRGQLIEDVEHTFEIEKPLYEHL 240

QY 241 HAYVRKLMNAYPSYISPIGCLPAHLGDMWGRFNTNLSLTVPFGOKNIDVTAMVDQ 300
Db 241 HAYVRKLMNAYPSYISPIGCLPAHLGDMWGRFNTNLSLTVPFGOKNIDVTAMVDQ 300

QY 301 AWAQRIEKEAEKFFVSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAMDGLKGFRIIM 360
Db 301 AWAQRIEKEAEKFFVSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAMDGLKGFRIIM 360
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301 ANAQRIFKEAEKFFVSVGLPNTQGFWNSMLTDFGNVQKAVCHTAWDLGKDFRILM 360
361 CTKVTDMDFFTAHEMGGHIQYDMAYAAQPFLLRNGANEGHEAVGEIMSLSAATPKHLKS 420
361 CTKVTDMDFFTAHEMGGHIQYDMAYAAQPFLLRNGANEGHEAVGEIMSLSAATPKHLKS 420
421 IGLSPDFQEDNTEINFLKQALTIIVGTLPTFYMLEKRWVFKGEIPKQDMKKWEM 480
421 IGLSPDFQEDNTEINFLKQALTIIVGTLPTFYMLEKRWVFKGEIPKQDMKKWEM 480
481 KREIVGVVPEVPHDTEYCDPASLFHVSNDYSFIRYTRTYLQFQOEALQAAKHGPHLH 540
481 KREIVGVVPEVPHDTEYCDPASLFHVSNDYSFIRYTRTYLQFQOEALQAAKHGPHLH 540
541 KCDISNSTEAGOKLFNMLRGKSEPTLALENVVGAKNMVRPLNLYFELPTWLDQNK 600
541 KCDISNSTEAGOKLFNMLRGKSEPTLALENVVGAKNMVRPLNLYFELPTWLDQNK 600
601 NSFVGMSTDSPPYADQSIKVRISLSKALGDKAYEWNDNEMYLFRSSVAYAMROYFLKVN 660
601 NSFVGMSTDSPPYADQSIKVRISLSKALGDKAYEWNDNEMYLFRSSVAYAMROYFLKVN 660
661 QMILFGEDVRVANLKRISNFVFTAPKNVSDIIPRTEVEKAIKRSRINDAFRLNDN 720
661 QMILFGEDVRVANLKRISNFVFTAPKNVSDIIPRTEVEKAIKRSRINDAFRLNDN 720
721 SLEFLGIQPTLGPNNQPPVSIWLVFVGMGVIYVGVILIFTGIRDKKKARSGENP 780
721 SLEFLGIQPTLGPNNQPPVSIWLVFVGMGVIYVGVILIFTGIRDKKKARSGENP 780
781 YASIDISKGNNPQFNTDDVQTSF 805
781 YASIDISKGNNPQFNTDDVQTSF 805

RESULT 7
US-09-969-384-13
; Sequence 13, Application US/09969384
; Publication No. US20020192749A1
; GENERAL INFORMATION:
; APPLICANT: Moore, et al.
; TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
; CURRENT APPLICATION NUMBER: US/09/969,384
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10542
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/236,384
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/194,118
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in ver. 2.0
; SEQ ID NO 13
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (219)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (240)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (499)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-969-384-13

Query Match 88.0%; Score 3775; DB 10; Length 711;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 704; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

62 MNAGDKWSAFLKEOSTLAOMYPLQEIQNLTKVLOQALQONGSSVLSEDSKRLNTILN 121
1 MNAGDKWSAFLKEOSTLAOMYPLQEIQNLTKVLOQALQONGSSVLSEDSKRLNTILN 60
122 TMTSTIYTGKVCNPNPOBCLLLEPGLNEIMANSLDYNRLWAWESWRSEYVKQLRPLYE 181
61 TMTSTIYTGKVCNPNPOBCLLLEPGLNEIMANSLDYNRLWAWESWRSEYVKQLRPLYE 120
182 EVVVLKNEAMARAHYEDYDGYRGGDYEVNGVDGYDYSRGQLIEDVEHTFEIKPLYEHLH 241
121 EVVVLKNEAMARAHYEDYDGYRGGDYEVNGVDGYDYSRGQLIEDVEHTFEIKPLYEHLH 180
242 AYVRAKLANVAPSYTSPICGLPAHLGDMGRFNTNLYSLTVPGQKPNIDVTAMVDOA 301
181 AYVRAKLANVAPSYTSPICGLPAHLGDMGRFNTNLYSLTVPGQKPNIDVTAMVDOX 240
302 WDAQRIFEAEKFFVSVGLPNTQGFWNSMLTDFGNVQKAVCHTAWDLGKDFRILMC 361
241 WDAQRIFEAEKFFVSVGLPNTQGFWNSMLTDFGNVQKAVCHTAWDLGKDFRILMC 300
362 TKVTMDDELTAHEMGGHIQYDMAYAAQPFLLRNGANEGHEAVGEIMSLSAATPKHLKSI 421
301 TKVTMDDELTAHEMGGHIQYDMAYAAQPFLLRNGANEGHEAVGEIMSLSAATPKHLKSI 360
422 GLLSPDFQEDNTEINFLKQALTIIVGTLPTFYMLEKRWVFKGEIPKQDMKKWEMK 481
361 GLLSPDFQEDNTEINFLKQALTIIVGTLPTFYMLEKRWVFKGEIPKQDMKKWEMK 420
482 REIVGVVPEVPHDTEYCDPASLFHVSNDYSFIRYTRTYLQFQOEALQAAKHGPHLH 541
421 REIVGVVPEVPHDTEYCDPASLFHVSNDYSFIRYTRTYLQFQOEALQAAKHGPHLH 480
542 CDISNSTEAGOKLFNMLRGKSEPTLALENVVGAKNMVRPLNLYFELPTWLDQNK 601
481 CDISNSTEAGOKLFNMLRGKSEPTLALENVVGAKNMVRPLNLYFELPTWLDQNK 540
602 SFVGMSTDSPPYADQSIKVRISLSKALGDKAYEWNDNEMYLFRSSVAYAMROYFLKVNQ 661
541 SFVGMSTDSPPYADQSIKVRISLSKALGDKAYEWNDNEMYLFRSSVAYAMROYFLKVNQ 600
662 MILFGEDVRVANLKRISNFVFTAPKNVSDIIPRTEVEKAIKRSRINDAFRLNDN 721
601 MILFGEDVRVANLKRISNFVFTAPKNVSDIIPRTEVEKAIKRSRINDAFRLNDN 660
722 LEFLGIQPTLGPNNQPPVSIWLVFVGMGVIYVGVILIFTGIRDKK 770
661 LEFLGIQPTLGPNNQPPVSIWLVFVGMGVIYVGVILIFTGIRDKK 709

RESULT 8
US-10-158-825-138
; Sequence 138, Application US/10158825
; Publication No. US20030138894A1
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF555
; CURRENT APPLICATION NUMBER: US/10/158,825
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/294,976
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 138
; LENGTH: 711
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (219)..
; OTHER INFORMATION: Xaa equals any amino acid
; FEATURE:

NAME/KEY: MISC FEATURE
LOCATION: (240)...(240)
OTHER INFORMATION: Xaa equals any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (499)...(499)
OTHER INFORMATION: Xaa equals any amino acid
US-10-158-825-138

Query Match 88.0%; Score 3775; DB 12; Length 711;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 704; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 62 MNNAGDKWGAFLKEQSTLAQMYPLQEIQNLTVKLQALQOQNGSSVLSSEKSKRLNTILN 121
Db 1 MNNAGDKWGAFLKEQSTLAQMYPLQEIQNLTVKLQALQOQNGSSVLSSEKSKRLNTILN 60

Qy 122 TMSITYSTGKVCNPNQECLELLEPGLNEIMANSLDYNERLWAWESWSEVSKQLRPLYE 181
Db 61 TMSITYSTGKVCNPNQECLELLEPGLNEIMANSLDYNERLWAWESWSEVSKQLRPLYE 120

Qy 182 EYVVLKNEARAHNYEDYDYNRGDYEYVNGVDGYDSRGQLIEDVEHTFEEIKPLYEHLH 241
Db 121 EYVVLKNEARAHNYEDYDYNRGDYEYVNGVDGYDSRGQLIEDVEHTFEEIKPLYEHLH 180

Qy 242 AYVRKLMNAYPSYISPIGCLPAHLGDMWGRFTNLISLTVPFGQKPNIDVTDAWVDOA 301
Db 181 AYVRKLMNAYPSYISPIGCLPAHLGDMWGRFTNLISLTVPFGQKPNIDVTDAWVDOX 240

Qy 302 WDAQRIFKEAEKFFSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKDFRILMC 361
Db 241 WDAQRIFKEAEKFFSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKDFRILMC 300

Qy 362 TKVTMDDFLTAHHEMGHIQYDMAYAAQPPFLRNGANEGFHEAVGEIMSLSAATPKHLKSI 421
Db 301 TKVTMDDFLTAHHEMGHIQYDMAYAAQPPFLRNGANEGFHEAVGEIMSLSAATPKHLKSI 360

Qy 422 GLSPDFQEDNETEINFLLKQALTIYGTLPFTYMLEKRWMMVKGEIPKQDQWKKWEMK 481
Db 361 GLSPDFQEDNETEINFLLKQALTIYGTLPFTYMLEKRWMMVKGEIPKQDQWKKWEMK 420

Qy 482 REIVGVVPEVPHDETYCDPASLFHVSNDYSFIRYTRTLYQFQOEALCOAAKHGGLPHK 541
Db 421 REIVGVVPEVPHDETYCDPASLFHVSNDYSFIRYTRTLYQFQOEALCOAAKHGGLPHK 480

Qy 542 CDSNSTEAGOKLFNMLRGKSEPTLALENVVGAKNMVRPLLNYFEPLFTWLKDQKN 601
Db 481 CDSNSTEAGOKLFNMLRGKSEPTLALENVVGAKNMVRPLLNYFEPLFTWLKDQKN 540

Qy 602 SFVGSWTDSPYADQSIKVRISLSKALGDKAYEWNDNEMYLFRSSVAYAMROYFLKVNQ 661
Db 541 SFVGSWTDSPYADQSIKVRISLSKALGDKAYEWNDNEMYLFRSSVAYAMROYFLKVNQ 600

Qy 662 MILFGEDVRVANLKPRISENFVTPAKNVSDFIIPTEVEKAIMRSRINDAFRLNDS 721
Db 601 MILFGEDVRVANLKPRISENFVTPAKNVSDFIIPTEVEKAIMRSRINDAFRLNDS 660

Qy 722 LEFLGIQPTLGPNNQPPVSIWLVFGVMGVIVVGVIVILIFTGIRDRKK 770
Db 661 LEFLGIQPTLGPNNQPPVSIWLVFGVMGVIVVGVIVILIFTGIRDRKK 709

RESULT 9
US-10-158-847-138
Sequence 138, Application US/10158847
Publication No. US20030091557A1
GENERAL INFORMATION:
APPLICANT: Tom Parry et al.
TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
FILE REFERENCE: PF557
CURRENT APPLICATION NUMBER: US/10/158,847
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: 60/295,004

PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 158
SOFTWARE: PatentIn version 3.1
SEQ ID NO 138
LENGTH: 711
TYPE: PRT
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (219)...(219)
OTHER INFORMATION: Xaa equals any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (240)...(240)
OTHER INFORMATION: Xaa equals any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (499)...(499)
OTHER INFORMATION: Xaa equals any amino acid
US-10-158-847-138

Query Match 88.0%; Score 3775; DB 15; Length 711;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 704; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 62 MNNAGDKWGAFLKEQSTLAQMYPLQEIQNLTVKLQALQOQNGSSVLSSEKSKRLNTILN 121
Db 1 MNNAGDKWGAFLKEQSTLAQMYPLQEIQNLTVKLQALQOQNGSSVLSSEKSKRLNTILN 60

Qy 122 TMSITYSTGKVCNPNQECLELLEPGLNEIMANSLDYNERLWAWESWSEVSKQLRPLYE 181
Db 61 TMSITYSTGKVCNPNQECLELLEPGLNEIMANSLDYNERLWAWESWSEVSKQLRPLYE 120

Qy 182 EYVVLKNEARAHNYEDYDYNRGDYEYVNGVDGYDSRGQLIEDVEHTFEEIKPLYEHLH 241
Db 121 EYVVLKNEARAHNYEDYDYNRGDYEYVNGVDGYDSRGQLIEDVEHTFEEIKPLYEHLH 180

Qy 242 AYVRKLMNAYPSYISPIGCLPAHLGDMWGRFTNLISLTVPFGQKPNIDVTDAWVDOA 301
Db 181 AYVRKLMNAYPSYISPIGCLPAHLGDMWGRFTNLISLTVPFGQKPNIDVTDAWVDOX 240

Qy 302 WDAQRIFKEAEKFFSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKDFRILMC 361
Db 241 WDAQRIFKEAEKFFSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKDFRILMC 300

Qy 362 TKVTMDDFLTAHHEMGHIQYDMAYAAQPPFLRNGANEGFHEAVGEIMSLSAATPKHLKSI 421
Db 301 TKVTMDDFLTAHHEMGHIQYDMAYAAQPPFLRNGANEGFHEAVGEIMSLSAATPKHLKSI 360

Qy 422 GLSPDFQEDNETEINFLLKQALTIYGTLPFTYMLEKRWMMVKGEIPKQDQWKKWEMK 481
Db 361 GLSPDFQEDNETEINFLLKQALTIYGTLPFTYMLEKRWMMVKGEIPKQDQWKKWEMK 420

Qy 482 REIVGVVPEVPHDETYCDPASLFHVSNDYSFIRYTRTLYQFQOEALCOAAKHGGLPHK 541
Db 421 REIVGVVPEVPHDETYCDPASLFHVSNDYSFIRYTRTLYQFQOEALCOAAKHGGLPHK 480

Qy 542 CDSNSTEAGOKLFNMLRGKSEPTLALENVVGAKNMVRPLLNYFEPLFTWLKDQKN 601
Db 481 CDSNSTEAGOKLFNMLRGKSEPTLALENVVGAKNMVRPLLNYFEPLFTWLKDQKN 540

Qy 602 SFVGSWTDSPYADQSIKVRISLSKALGDKAYEWNDNEMYLFRSSVAYAMROYFLKVNQ 661
Db 541 SFVGSWTDSPYADQSIKVRISLSKALGDKAYEWNDNEMYLFRSSVAYAMROYFLKVNQ 600

Qy 662 MILFGEDVRVANLKPRISENFVTPAKNVSDFIIPTEVEKAIMRSRINDAFRLNDS 721
Db 601 MILFGEDVRVANLKPRISENFVTPAKNVSDFIIPTEVEKAIMRSRINDAFRLNDS 660

Qy 722 LEFLGIQPTLGPNNQPPVSIWLVFGVMGVIVVGVIVILIFTGIRDRKK 770
Db 661 LEFLGIQPTLGPNNQPPVSIWLVFGVMGVIVVGVIVILIFTGIRDRKK 709

RESULT 10
US-09-969-384-25
; Sequence 25, Application US/09969384
; Publication No. US20020192749A1
; GENERAL INFORMATION:
; APPLICANT: Moore, et al.
; TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT055P1
; CURRENT APPLICATION NUMBER: US/09/969,384
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10542
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/236,384
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/194,118
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (219)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (240)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (499)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-969-384-25

Query Match 84.9%; Score 3643; DB 10; Length 681;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 676; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 62 MNNAGDKWSAFLEKQSTLAQMPLOEIQNLTVKLOLQALQONGSSVLSSEKSKRLNTILN 121
Db 1 MNNAGDKWSAFLEKQSTLAQMPLOEIQNLTVKLOLQALQONGSSVLSSEKSKRLNTILN 60

Qy 122 TMSTIYSTGKVCNPNPQECILLPEGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 181
Db 61 TMSTIYSTGKVCNPNPQECILLPEGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 120

Qy 182 EYVVLKNEAMARANHVEDYGYWRGDIYVNGVDYSGQLIEDVEHTFEIKPLYEHLH 241
Db 121 EYVVLKNEAMARANHVEDYGYWRGDIYVNGVDYSGQLIEDVEHTFEIKPLYEHLH 180

Qy 242 AYVRAKLMNAYPSYISPIGCLPAHLGDMGGRFNTNLYSLTVFPQKPNIDVTDAMVDQA 301
Db 181 AYVRAKLMNAYPSYISPIGCLPAHLGDMGGRFNTNLYSLTVFPQKPNIDVTDAMVDQA 240

Qy 302 WDAQRIFKEAEKFFVSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRLIMC 361
Db 241 WDAQRIFKEAEKFFVSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRLIMC 300

Qy 362 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 421
Db 301 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 360

Qy 422 GLLSPDFQEDNETEINFLLKQALITVGTLPPTYMLEKRWNVFKGEIPKQWKKWEMK 481
Db 361 GLLSPDFQEDNETEINFLLKQALITVGTLPPTYMLEKRWNVFKGEIPKQWKKWEMK 420

Qy 482 REIVGVVEPVPHDETYCDPASLFVNSNDYSFIRYRTLYQFQEALCOAAKHEGGLHK 541
Db 421 REIVGVVEPVPHDETYCDPASLFVNSNDYSFIRYRTLYQFQEALCOAAKHEGGLHK 480

Qy 542 CDISNSTEAGOKLFNMLRKXKSEPTWLTALENVVGAKNVVRPLINYPPELFTWLKDQKN 601

Db 481 CDISNSTEAGOKLFNMLRKXKSEPTWLTALENVVGAKNVVRPLINYPPELFTWLKDQKN 540

Qy 602 SFVGMSTDSYADQSIKVRISLKSALGDKAYENNDNEMYLFRSSVAYAVRQYPLKVKNQ 661
Db 541 SFVGMSTDSYADQSIKVRISLKSALGDKAYENNDNEMYLFRSSVAYAVRQYPLKVKNQ 600

Qy 662 MILGGEEDVRANLKPRISENFVFTAPKNVSDIIPRTEVEKATMRSSRINDAFRLNDNS 721
Db 601 MILGGEEDVRANLKPRISENFVFTAPKNVSDIIPRTEVEKATMRSSRINDAFRLNDNS 660

Qy 722 LEFLGIQPTLGLPPNPQPPVSIW 742
Db 661 LEFLGIQPTLGLPPNPQPPVSIW 681

RESULT 11
US-10-158-825-140
; Sequence 140, Application US/10158825
; Publication No. US20030138894A1
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PFS55
; CURRENT APPLICATION NUMBER: US/10/158,825
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/294,976
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 140
; LENGTH: 681
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (219)-(219)
; OTHER INFORMATION: Xaa equals any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (240)-(240)
; OTHER INFORMATION: Xaa equals any amino acid
; NAME/KEY: MISC FEATURE
; LOCATION: (499)-(499)
; OTHER INFORMATION: Xaa equals any amino acid
US-10-158-825-140

Query Match 84.9%; Score 3643; DB 12; Length 681;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 676; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 62 MNNAGDKWSAFLEKQSTLAQMPLOEIQNLTVKLOLQALQONGSSVLSSEKSKRLNTILN 121
Db 1 MNNAGDKWSAFLEKQSTLAQMPLOEIQNLTVKLOLQALQONGSSVLSSEKSKRLNTILN 60

Qy 122 TMSTIYSTGKVCNPNPQECILLPEGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 181
Db 61 TMSTIYSTGKVCNPNPQECILLPEGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 120

Qy 182 EYVVLKNEAMARANHVEDYGYWRGDIYVNGVDYSGQLIEDVEHTFEIKPLYEHLH 241
Db 121 EYVVLKNEAMARANHVEDYGYWRGDIYVNGVDYSGQLIEDVEHTFEIKPLYEHLH 180

Qy 242 AYVRAKLMNAYPSYISPIGCLPAHLGDMGGRFNTNLYSLTVFPQKPNIDVTDAMVDQA 301
Db 181 AYVRAKLMNAYPSYISPIGCLPAHLGDMGGRFNTNLYSLTVFPQKPNIDVTDAMVDQA 240

Qy 302 WDAQRIFKEAEKFFVSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRLIMC 361
Db 241 WDAQRIFKEAEKFFVSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRLIMC 300

Qy 362 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 421
Db 301 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 360

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Db 301 TKVTMDDELTAHEMGIQYDMAYAAQFFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 360
QY 422 GLLSPDFDQEDNETEINFLLKQALITVGLPTTYMLEKRWNVFKGEIPKQOMKKWEMK 481
Db 361 GLLSPDFDQEDNETEINFLLKQALITVGLPTTYMLEKRWNVFKGEIPKQOMKKWEMK 420
QY 482 REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYTRTYLQFQOEALCAAHEGFLHK 541
Db 421 REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYTRTYLQFQOEALCAAHEGFLHK 480
QY 542 CDISNSTEAGOKLFNMLRGKSEPTWTLALENVVGAKNVVRPLLNYPEPLFTWLKQONKN 601
Db 481 CDISNSTEAGOKLFNMLRGKSEPTWTLALENVVGAKNVVRPLLNYPEPLFTWLKQONKN 540
QY 602 SFVGSNTDWSPVADQSIKVRISLKSALGDKAYEWNNDNEMYLFRSSVAYAMQYFLKVKNQ 661
Db 541 SFVGSNTDWSPVADQSIKVRISLKSALGDKAYEWNNDNEMYLFRSSVAYAMQYFLKVKNQ 600
QY 662 MILFGEEDVRVANLKPRISENFVFTAPKNVSDIIPRTEVEKAIRMSRINDAFRLNDS 721
Db 601 MILFGEEDVRVANLKPRISENFVFTAPKNVSDIIPRTEVEKAIRMSRINDAFRLNDS 660
QY 722 LEFLGIQPTLGPNNQPPVSIW 742
Db 661 LEFLGIQPTLGPNNQPPVSIW 681

RESULT 12
US-10-158-847-140
; Sequence 140, Application US/10158847
; Publication No. US20030091557A1
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 140
; LENGTH: 681
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (219)..(219)
; OTHER INFORMATION: Xaa equals any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa equals any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (499)..(499)
; OTHER INFORMATION: Xaa equals any amino acid
US-10-158-847-140

Query Match 84.9%; Score 3643; DB 15; Length 681;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 676; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 62 MNNAGDKWSAFLKEQSTLAQMPYPIQETQNLTKVLQALQONGSSVLSEKSKRLNTILN 121
Db 1 MNNAGDKWSAFLKEQSTLAQMPYPIQETQNLTKVLQALQONGSSVLSEKSKRLNTILN 60
QY 122 TMSIYSTGKVCNPDNPEQCLLPGLNEINWANSLDYNERLWAWESRSEVQKOLRPLYE 181
Db 61 TMSIYSTGKVCNPDNPEQCLLPGLNEINWANSLDYNERLWAWESRSEVQKOLRPLYE 120
QY 182 EYVVLKQEMARANHVEDYDGRGDEYVNGVDYSGRGLIEDVEHTFEIKPLYEHLH 241
```

```
Db 121 EYVVLKQEMARANHVEDYDGRGDEYVNGVDYSGRGLIEDVEHTFEIKPLYEHLH 180
QY 242 AYVRAKLKMANPYSYISPIGCLPAHLGDMWGRFWTNLYSLTVPPFGQKPNIDVTDAWDOA 301
Db 181 AYVRAKLKMANPYSYISPIGCLPAHLGDMWGRFWTNLYSLTVPPFGQKPNIDVTDAWDOA 240
QY 302 WDAQRIFKEAEKFFSVGLPNMTQGFWSNMLTDFGNVQKAVCHPTANDLGKDFRILWC 361
Db 241 WDAQRIFKEAEKFFSVGLPNMTQGFWSNMLTDFGNVQKAVCHPTANDLGKDFRILWC 300
QY 362 TKVTWDDDLTAHEMGIQYDMAYAAQFFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 421
Db 301 TKVTWDDDLTAHEMGIQYDMAYAAQFFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 360
QY 422 GLLSPDFDQEDNETEINFLLKQALITVGLPTTYMLEKRWNVFKGEIPKQOMKKWEMK 481
Db 361 GLLSPDFDQEDNETEINFLLKQALITVGLPTTYMLEKRWNVFKGEIPKQOMKKWEMK 420
QY 482 REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYTRTYLQFQOEALCAAHEGFLHK 541
Db 421 REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYTRTYLQFQOEALCAAHEGFLHK 480
QY 542 CDISNSTEAGOKLFNMLRGKSEPTWTLALENVVGAKNVVRPLLNYPEPLFTWLKQONKN 601
Db 481 CDISNSTEAGOKLFNMLRGKSEPTWTLALENVVGAKNVVRPLLNYPEPLFTWLKQONKN 540
QY 602 SFVGSNTDWSPVADQSIKVRISLKSALGDKAYEWNNDNEMYLFRSSVAYAMQYFLKVKNQ 661
Db 541 SFVGSNTDWSPVADQSIKVRISLKSALGDKAYEWNNDNEMYLFRSSVAYAMQYFLKVKNQ 600
QY 662 MILFGEEDVRVANLKPRISENFVFTAPKNVSDIIPRTEVEKAIRMSRINDAFRLNDS 721
Db 601 MILFGEEDVRVANLKPRISENFVFTAPKNVSDIIPRTEVEKAIRMSRINDAFRLNDS 660
QY 722 LEFLGIQPTLGPNNQPPVSIW 742
Db 661 LEFLGIQPTLGPNNQPPVSIW 681

RESULT 13
US-09-978-385-6
; Sequence 6, Application US/09978385
; Patent No. US20020177211A1
; GENERAL INFORMATION:
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Petrie, Charles
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME
; FILE REFERENCE: 99-24C1
; CURRENT APPLICATION NUMBER: US/09/978,385
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/133,952
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/151,181
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 09/563,516
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Mouse
US-09-978-385-6

Query Match 83.4%; Score 3579; DB 10; Length 805;
Best Local Similarity 82.1%; Pred. No. 0;
Matches 661; Conservative 60; Mismatches 84; Indels 0; Gaps 0;

QY 1 MSSSWLLLSLVAVTAAQSTIEQAKTFLDFKFNHEADLFYQSSLASNNYNTNITEENVQ 60
Db 1 MSSSWLLLSLVAVTAAQSTIEQAKTFLDFKFNHEADLFYQSSLASNNYNTNITEENAQ 60
```

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QY 61 NMNAGDKWSAFLEKEOSTLAQMPLOEIONLTVKLOLQALQONGSSVLSEDKSRINTIL 120
DB 61 KMSEAAKWSAFYEQSKTAQSFSLQEIQTPIIKRQLOALQOQSSALSADKNKQNTIL 120
QY 121 NTMSTIYSTGKVCNPNQPCQLLEPGLNEIMANSLDYNERLWAWESRSEVQKQLRPLY 180
DB 121 NTMSTIYSTGKVCNPNQPCQLLEPGLDEIMATSTDYNSRLWAWEGRAEVQKQLRPLY 180
QY 181 EBYVVLKNEMARANHYEDYDYGWGDYEVNGVDGYDSRGQLIEDVEHTFEEIKPLYEHL 240
DB 181 EBYVVLKNEMARANNYNDYDYGWGDYEAEGADGYNNENQLIEDVERTFAEIKPLYEHL 240
QY 241 HAYVRAKLMMNAYSYSPIGCLPAHLGDMWGRFWNLXSLTVFPQKPNIDVTDAMVQ 300
DB 241 HAYVRKLMDTYPSISPTGCLPAHLGDMWGRFWNLXSLTVFPQKPNIDVTDAMNQ 300
QY 301 AWDAQRIKFAEKFPVSGLPNTQGFWNSMLTDGPNVQKAVCHPTAMDGLGKDFRILM 360
DB 301 GWAERIFQEAERKFVSGLPHTQGFWNSMLTEPADGRKVVCHPTAMDGLHGDFRILM 360
QY 361 CTKVTMDDFLTAHEMIGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
DB 361 CTKVTMDNFLTAAHEMIGHIQYDMAYARQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
QY 421 IGLLSPDFQEDNETEINFLKQALTIYGTLPFTYMLEKRWMMVFKGEIPKQOMKKWEM 480
DB 421 IGLLSPDFQEDSETEINFLKQALTIYGTLPFTYMLEKRWMMVFRGEIPKQOMKKWEM 480
QY 481 KREIVGVVPEPHDTEYCDPASLFHVSNDYSFIRYTRTYQFQOEALCOAAKHEGPLH 540
DB 481 KREIVGVVPELPHDTEYCDPASLFHVSNDYSFIRYTRTYQFQOEALCOAAKNGSLH 540
QY 541 KCDISNSTEAGQKLFNMLRKSEPPWTALENVVGAQNMVRLNLYFELFTWLKQDNK 600
DB 541 KCDISNSTEAGQKLLKMLSLGNSEPPWTKALENVVGAENMDVKPLNYFQPLFDMLEQNR 600
QY 601 NSFVGMSTDSPYADQSIKVRISLKSALGDKAYEWNNDNEMYLFRSSVAYAMROYFLKVK 660
DB 601 NSFVGMSTWSPYADQSIKVRISLKSALGANAYEWNNDNEMFLFRSSVAYAMRYFIIKN 660
QY 661 QMILFGBEDVRVANLKPRISNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLND 720
DB 661 QTVPFLEEDVRVSDLKPRVSFYFVTSPQNVSDVPRSEVEDAIRMSRGRINDVFGIND 720
QY 721 SLEFLGIQPLTPNQPVSFWLVGVVGMVIVGVVILIFTGIRDRKKKKARSGENP 780
DB 721 SLEFLGIHTLEPPYQPPVTIWLIFGVVVALVVVGIILITVGIKGRKKKNETKREENP 780
QY 781 YASIDISKGENNPGFQNTDDVQTSF 805
DB 781 YDSMDIGKESNAGFQNSDDAQTSE 805
```

RESULT 14

```
US-09-978-385-9
; Sequence 9, Application US/09978385
; Patent No. US20020177211A1
; GENERAL INFORMATION:
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Petrie, Charles
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME
; FILE REFERENCE: 99-24C1
; CURRENT APPLICATION NUMBER: US/09/978,385
; CURRENT FILING DATE: 2001-10-15
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/133,952
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/151,181
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/563,516
```

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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Mouse
US-09-978-385-9
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Query Match 83.0%; Score 3561; DB 10; Length 805;
Best Local Similarity 81.9%; Pred. No. 7,3e-317;
Matches 559; Conservative 60; Mismatches 86; Indels 0; Gaps 0;
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QY 1 MSSSSWLLLSLVATAAQSTIEBOAKTFLDKFHEAEDLFVQSSLASWNTNTITEENVO 60
DB 1 MSSSSWLLLSLVATAAQSTIEENAKTFLANNFNOEADLSYQSSLASWNTNTITEENAQ 60
QY 61 NMNAGDKWSAFLEKEOSTLAQMPLOEIONLTVKLOLQALQONGSSVLSEDKSRINTIL 120
DB 61 KMSEAAKWSAFYEQSKTAQSFSLQEIQTPIIKRQLOALQOQSSALSADKNKQNTIL 120
QY 121 NTMSTIYSTGKVCNPNQPCQLLEPGLNEIMANSLDYNERLWAWESRSEVQKQLRPLY 180
DB 121 NTMSTIYSTGKVCNPNQPCQLLEPGLDEIMATSTDYNSRLWAWEGRAEVQKQLRPLY 180
QY 181 EBYVVLKNEMARANHYEDYDYGWGDYEVNGVDGYDSRGQLIEDVEHTFEEIKPLYEHL 240
DB 181 EBYVVLKNEMARANNYNDYDYGWGDYEAEGADGYNNENQLIEDVERTFAEIKPLYEHL 240
QY 241 HAYVRAKLMMNAYSYSPIGCLPAHLGDMWGRFWNLXSLTVFPQKPNIDVTDAMVQ 300
DB 241 HAYVRKLMDTYPSISPTGCLPAHLGDMWGRFWNLXSLTVFPQKPNIDVTDAMNQ 300
QY 301 AWDAQRIKFAEKFPVSGLPNTQGFWNSMLTDGPNVQKAVCHPTAMDGLGKDFRILM 360
DB 301 GWAERIFQEAERKFVSGLPHTQGFWNSMLTEPADGRKVVCHPTAMDGLHGDFRILM 360
QY 361 CTKVTMDDFLTAHEMIGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
DB 361 CTKVTMDNFLTAAHEMIGHIQYDMAYARQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
QY 421 IGLLSPDFQEDNETEINFLKQALTIYGTLPFTYMLEKRWMMVFKGEIPKQOMKKWEM 480
DB 421 IGLLSPDFQEDSETEINFLKQALTIYGTLPFTYMLEKRWMMVFRGEIPKQOMKKWEM 480
QY 481 KREIVGVVPEPHDTEYCDPASLFHVSNDYSFIRYTRTYQFQOEALCOAAKHEGPLH 540
DB 481 KREIVGVVPELPHDTEYCDPASLFHVSNDYSFIRYTRTYQFQOEALCOAAKNGSLH 540
QY 541 KCDISNSTEAGQKLFNMLRKSEPPWTALENVVGAQNMVRLNLYFELFTWLKQDNK 600
DB 541 KCDISNSTEAGQKLLKMLSLGNSEPPWTKALENVVGAENMDVKPLNYFQPLFDMLEQNR 600
QY 601 NSFVGMSTDSPYADQSIKVRISLKSALGDKAYEWNNDNEMYLFRSSVAYAMROYFLKVK 660
DB 601 NSFVGMSTWSPYADQSIKVRISLKSALGANAYEWNNDNEMFLFRSSVAYAMRYFIIKN 660
QY 661 QMILFGBEDVRVANLKPRISNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLND 720
DB 661 QTVPFLEEDVRVSDLKPRVSFYFVTSPQNVSDVPRSEVEDAIRMSRGRINDVFGIND 720
QY 721 SLEFLGIQPLTPNQPVSFWLVGVVGMVIVGVVILIFTGIRDRKKKKARSGENP 780
DB 721 SLEFLGIHTLEPPYQPPVTIWLIFGVVVALVVVGIILITVGIKGRKKKNETKREENP 780
QY 781 YASIDISKGENNPGFQNTDDVQTSF 805
DB 781 YDSMDIGKESNAGFQNSDDAQTSE 805
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RESULT 15

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US-10-137-870-72
; Sequence 72, Application US/10137870
; Publication No. US2003013883A1
```

GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC155
; CURRENT APPLICATION NUMBER: US/10/137,870
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 72
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-870-72

Query Match 69.4%; Score 2979; DB 12; Length 555;
Best Local Similarity 99.8%; Pred. No. 8,6e-264;
Matches 553; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFDKFNHEAEADLFYQSSLASWNYNTNITEENVQ 60
DB 1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFDKFNHEAEADLFYQSSLASWNYNTNITEENVQ 60
QY 61 NMNAGDKWSAFLEKQSTLAQMYPLQEIQNTLVKLQALQONGSSVLSEDKSKRLNTIL 120
DB 61 NMNAGDKWSAFLEKQSTLAQMYPLQEIQNTLVKLQALQONGSSVLSEDKSKRLNTIL 120
QY 121 NTMSTIYTGKVCNPDNPOECULLBPGLEINMANSLDYNERLWAWESWRSEVGKQLRPLY 180
DB 121 NTMSTIYTGKVCNPDNPOECULLBPGLEINMANSLDYNERLWAWESWRSEVGKQLRPLY 180
QY 181 EBYVVLKNEMARANHYEDYDWRGDYEVNGVDYDYSRGQLIEDVHTFEEIKPLYEHL 240
DB 181 EBYVVLKNEMARANHYEDYDWRGDYEVNGVDYDYSRGQLIEDVHTFEEIKPLYEHL 240
QY 241 HAYVRAKLMNAYPSYISPIGCLPAHLGLDMGCRFWTNLYSLTVPGQKPNIDVTDAMVDQ 300
DB 241 HAYVRAKLMNAYPSYISPIGCLPAHLGLDMGCRFWTNLYSLTVPGQKPNIDVTDAMVDQ 300
QY 301 AMDAQRIFYKEAEKFFVSVGLPNNTOGFWNSMLTDPGNVQKAVCHPTAWDLKGDFFRLM 360
DB 301 AMDAQRIFYKEAEKFFVSVGLPNNTOGFWNSMLTDPGNVQKAVCHPTAWDLKGDFFRLM 360
QY 361 CTKTVMDDFLTAHHENGHIQYDMAYAAQPFLLRNGANEGFHAUGEIMSLSAATPKHLKS 420
DB 361 CTKTVMDDFLTAHHENGHIQYDMAYAAQPFLLRNGANEGFHAUGEIMSLSAATPKHLKS 420
QY 421 IGLSPDFQEDNTEINFLKQALTIIVGLPTMYLKWVWVFKGEIPKQOMKKWEM 480
DB 421 IGLSPDFQEDNTEINFLKQALTIIVGLPTMYLKWVWVFKGEIPKQOMKKWEM 480
QY 481 KREIVGVPEVPHEDEYCDPASLFHVSNDYSFIRYVTRTYQFQCEALCQAAKHEGPLH 540
DB 481 KREIVGVPEVPHEDEYCDPASLFHVSDDYSFIRYVTRTYQFQCEALCQAAKHEGPLH 540
QY 541 KCDISNSTEAGQKL 554
|||||

DB 541 KCDISNSTEAGQKL 554

Search completed: February 19, 2004, 19:53:06

Job time : 42 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 19, 2004, 19:47:18 ; Search time 41 Seconds
(without alignments)
5066.643 Million cell updates/sec

Title: US-09-163-648-2

Perfect score: 4291
Sequence: 1 MSSSWLLSLVAVTAAGT.....ISKGNPQFQNTDDVQTSF 805

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_invertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4291	100.0	805	4 Q9NRA7	Q9nra7 homo sapien
2	4288	99.9	805	4 Q9YF1	Q9yfi1 homo sapien
3	4281	99.8	804	4 Q9UF26	Q9ufz6 homo sapien
4	3579	83.4	805	11 Q8R010	Q8r010 mus musculus
5	3485	81.2	798	11 Q9N71	Q9n71 mus musculus
6	1539	35.9	353	11 Q9N70	Q9n70 mus musculus
7	1347.5	31.4	739	4 Q9N70	Q9n70 homo sapien
8	1336	31.1	732	6 Q9GLN6	Q9glh6 pan troglod
9	1334	31.1	1015	11 Q8K233	Q8k233 mus musculus
10	1329	31.0	1304	6 Q9GLN7	Q9glh7 pan troglod
11	1310	30.5	775	11 Q8CFN1	Q8cfni rattus norv
12	1310	30.5	1313	11 Q9EOM9	Q9eqm9 rattus norv
13	1303	30.4	694	4 Q15540	Q15540 homo sapien
14	1100.5	25.6	619	16 Q8EE33	Q8ee33 shewanella
15	1089.5	25.4	648	5 Q9ND88	Q9nds8 bombyx mori
16	1071	25.0	265	11 Q9D836	Q9d836 mus musculus

ALIGNMENTS

RESULT 1

ID	Q9NRA7	PRELIMINARY;	PRT;	805 AA.
AC	Q9NRA7;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Angiotensin converting enzyme-like protein (ACE-related carboxypeptidase ACE2).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lymphoma;			
RA	Tipnis S.R.; Hooper N.M.; Hyde R.J.; Christie G.; Karran E.,			
RA	Turner A.J.;			
RT	"A Human Homolog of Angiotensin Converting Enzyme - Cloning and Functional Expression As A Captopril-Insensitive Carboxypeptidase."			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Donoghue M., Hsieh F., Baronas E., Godbout K., Gosselin M.,			
RA	Stagliano N., Donovan M., Woolf B., Robison K., Jeyaseelan R.,			
RA	Breitbart R.E.; Acton S.;			
RT	"A novel ACE-related carboxypeptidase (ACE2) converts angiotensin I to angiotensin1-9."			
RL	Circ. Res. 0:0-0(2000).			
DR	EMBL; AF241254; AAF78220.1; -			
DR	EMBL; AF291820; AAF99721.1; -			
DR	MEROPS; M02.006; -			
DR	InterPro; IPR001548; Peptidase_M2.			
DR	InterPro; IPR006025; Zn_MpPeptdse.			
DR	Pfam; PF01401; Peptidase_M2; 1.			
DR	PRINTS; PR00791; PEPDPTASEA.			
DR	ProDom; PD004184; Peptidase_M2; 1.			
DR	PROSITE; PS00142; ZINC_PROTEASE; 1.			
KW	Carboxypeptidase.			

17	1057	24.6	660	5	Q17248
18	1030	24.0	630	5	Q24222
19	1028	24.0	630	5	Q9VLJ6
20	968.5	22.6	672	16	Q8PN56
21	967	22.5	672	16	Q8PBK3
22	930	21.7	844	5	Q8SXX2
23	737	17.2	674	5	Q9VJV1
24	641	14.9	906	5	Q18581
25	500.5	11.7	609	5	Q9V520
26	500.5	11.7	620	5	Q8MS05
27	476	11.1	611	5	Q9VJV2
28	434.5	10.1	202	11	Q64603
29	403.5	9.5	628	5	Q3W021
30	408.5	9.5	628	5	Q9SUS9
31	390	9.1	222	11	Q9ESG3
32	387	9.0	222	4	Q9HBJ8
33	386	9.0	222	11	Q9ESG4
34	306.5	7.1	121	6	Q9BDG1
35	280.5	6.5	135	4	Q16425
36	251.5	5.9	157	11	Q61265
37	171.5	4.0	154	5	Q8IP60
38	157	3.7	532	16	Q9KPV0
39	154	3.6	502	16	Q8Y616
40	152.5	3.6	734	5	Q9NKE3
41	147	3.4	54	6	Q9S161
42	147	3.4	502	16	Q92AC3
43	139.5	3.3	987	16	Q8YWG6
44	139	3.2	608	16	Q9PR80
45	138.5	3.2	613	16	Q8D839

Q17248	boophilus m
Q24222	drosophila
Q9VLJ6	drosophila
Q8PN56	xanthomonas
Q8PBK3	xanthomonas
Q8SXX2	drosophila
Q9VJV1	drosophila
Q18581	caenorhabdi
Q9V520	drosophila
Q8MS05	drosophila
Q9VJV2	drosophila
Q64603	rattus norv
Q3W021	drosophila
Q9SUS9	drosophila
Q9ESG3	rattus norv
Q9HBJ8	homo sapien
Q9ESG4	mus musculu
Q9BDG1	bos taurus
Q16425	homo sapien
Q61265	mus musculu
Q8IP60	drosophila
Q9KPV0	bacillus ba
Q8Y616	listeria mo
Q9NKE3	drosophila
Q9S161	canis fami
Q92AC3	listeria in
Q8YWG6	anabaena sp
Q9PR80	ureaplasma
Q8D839	vibrio vuln


```
Db 661 QMLFGEEDVRVANLKPRISFNFFVTAPKNVSDIIIPRTEVEKAIMRSRINDAFRLNDN 720
Qy 721 SLBFLGIQPTLGPNNQPPVSIWLVFGVVMGVIVGIVILITPTGIDRKKKKKARSGENP 780
Db 721 SLBFLGIQPTLGPNNQPPVSIWLVFGVVMGVIVGIVILITPTGIDRKKKKKARSGENP 780
Qy 781 YASIDISKGENNPGFQNTDDVQTSF 805
Db 781 YASIDISKGENNPGFQNTDDVQTSF 805

RESULT 3
Q9UFZ6 PRELIMINARY; PRT; 804 AA.
ID Q9UFZ6
AC Q9UFZ6
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFZP434A014.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL110224; CAB53682.1; -.
DR MEROPS; M02.006; -.
DR InterPro; IPR001548; Peptidase M2.
DR InterPro; IPR006025; Zn_MTPeptidse.
DR Pfam; PF01401; Peptidase M2; 1.
DR PRINTS; PR00791; PEPDPTASEA.
DR ProDom; PD004184; Peptidase M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 804 AA; 92340 MW; 91FF391074CB5DA9 CRC64;

Query Match 99.8%; Score 4281; DB 4; Length 804;
Best Local Similarity 99.9%; Pred. No. 7.9e-308;
Matches 803; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SSSSWLLLSLVAVTAQAQSTIEEQAKTFLDKENHEAEDLFYQSSLASWNYNTNITEENVQ 61
Db 1 SSSSWLLLSLVAVTAQAQSTIEEQAKTFLDKENHEAEDLFYQSSLASWNYNTNITEENVQ 60
Qy 62 MNAGDKWSAFLEKQSTLAQMYPLQEIQNLTQVQLQALQNGSSVLSDEKSKRLNTILN 121
Db 61 MNAGDKWSAFLEKQSTLAQMYPLQEIQNLTQVQLQALQNGSSVLSDEKSKRLNTILN 120
Qy 122 TMSITYSTGKVCNPDNPQECILLBPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLYE 181
Db 121 TMSITYSTGKVCNPDNPQECILLBPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLYE 180
Qy 182 EYVVLKNEARANHYEDYDWRGDEYVNGVDYDYSRGQLIEDVHTFEEIKPLYEHLH 241
Db 181 EYVVLKNEARANHYEDYDWRGDEYVNGVDYDYSRGQLIEDVHTFEEIKPLYEHLH 240
Qy 242 AYVRAKLMNVPYSISPICGLPAHLGDMWGRFNTNLYSLTPVGQKPNIDVTDMYDQA 301
Db 241 AYVRAKLMNVPYSISPICGLPAHLGDMWGRFNTNLYSLTPVGQKPNIDVTDMYDQA 300
Qy 302 WDAQRIPEAEKFFVSVGLPNWTOGFWNSMLTDPGNVQKAVCHPTADLKGDFRILMC 361
Db 301 WDAQRIPEAEKFFVSVGLPNWTOGFWNSMLTDPGNVQKAVCHPTADLKGDFRILMC 360
Qy 362 TKVTMDDFLTARHENGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 421
Db 361 TKVTMDDFLTARHENGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 420
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Qy 422 GLLSPDFOEDNETEINFLKQALTIIVGTLPTFTYMLEKRWVWVFKGEIPKQDQWKKWEMK 481
Db 421 GLLSPDFOEDNETEINFLKQALTIIVGTLPTFTYMLEKRWVWVFKGEIPKQDQWKKWEMK 480
Qy 482 REIVGVVEVPVPHDFTYCDPASLPHVSNDSYFIRYTYTTLTYQFOEALCOAAKHEGPLHK 541
Db 481 REIVGVVEVPVPHDFTYCDPASLPHVSNDSYFIRYTYTTLTYQFOEALCOAAKHEGPLHK 540
Qy 542 CDISNSTEAGOKLFNMLRLGKSEPTWTLALENVVGAKNNVRLPLNYPEPLFTWLKDQKN 601
Db 541 CDISNSTEAGOKLFNMLRLGKSEPTWTLALENVVGAKNNVRLPLNYPEPLFTWLKDQKN 600
Qy 602 SFVGNSTDWSPYADQSKIVRISLSKALGDKAYENDNENYLFSSVAYANROYELKVKNQ 661
Db 601 SFVGNSTDWSPYADQSKIVRISLSKALGDKAYENDNENYLFSSVAYANROYELKVKNQ 660
Qy 662 MILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIIPRTEVEKAIMRSRINDAFRLNDNS 721
Db 661 MILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIIPRTEVEKAIMRSRINDAFRLNDNS 720
Qy 722 LEFTGIQPTLGPNNQPPVSIWLVFGVVMGVIVGIVILITPTGIDRKKKKKARSGENPY 781
Db 721 LEFTGIQPTLGPNNQPPVSIWLVFGVVMGVIVGIVILITPTGIDRKKKKKARSGENPY 780
Qy 782 ASIDISKGENNPGFQNTDDVQTSF 805
Db 781 ASIDISKGENNPGFQNTDDVQTSF 804

RESULT 4
Q8RO10 PRELIMINARY; PRT; 805 AA.
ID Q8RO10
AC Q8RO10
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE RIKEN cDNA 2010305L05 gene.
GN ACE2 OR 2010305L05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026801; AAH26801.1; -.
DR MGD; MGI:1917258; Ace2.
DR InterPro; IPR001548; Peptidase M2.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR006025; Zn_MTPeptidse.
DR Pfam; PF01401; Peptidase M2; 1.
DR ProDom; PD004184; Peptidase M2; 1.
DR PROSITE; PS00678; WD_REPEATS; 1.
DR PROSITE; PS00442; ZINC_PROTEASE; 1.
SQ SEQUENCE 805 AA; 92367 MW; D8B883AAC966A8D9 CRC64;
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Query Match 83.4%; Score 3579; DB 11; Length 805;
Best Local Similarity 82.1%; Pred. No. 6.6e-256;
Matches 661; Conservative 60; Mismatches 84; Indels 0; Gaps 0;

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Qy 1 MSSSWLLLSLVAVTAQAQSTIEEQAKTFLDKENHEAEDLFYQSSLASWNYNTNITEENVQ 60
Db 1 MSSSWLLLSLVAVTAQAQSTIEEQAKTFLDKENHEAEDLFYQSSLASWNYNTNITEENVQ 60
Qy 61 MNAGDKWSAFLEKQSTLAQMYPLQEIQNLTQVQLQALQNGSSVLSDEKSKRLNTIL 120
Db 61 MNAGDKWSAFLEKQSTLAQMYPLQEIQNLTQVQLQALQNGSSVLSDEKSKRLNTIL 120
Qy 121 TMSITYSTGKVCNPDNPQECILLBPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180
Db 121 TMSITYSTGKVCNPDNPQECILLBPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180
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DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anigotensin-converting enzyme-related carboxypeptidase.
GN ACE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Komatsu T., Sugano S., Imai J., Suzuki Y., Hanaoka K., Yamada Y.,
RA Hida M., Tanigami A., Muroi S.;
RT "Molecular cloning, mRNA expression, and chromosomal localization of
RT mouse Angiotensin-converting Enzyme-Related Carboxypeptidase.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Komatsu T., Sugano S., Suzuki Y., Hanaoka K., Yamada Y.;
RT "Molecular cloning of ACE2.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB053182; BAB40432.1; -
DR MEROPS; M02.006; -.
DR MGD; MGI:1917258; Ace2.
DR InterPro; IPR001548; Peptidase_M2.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; PEPDIPASEA.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
DR Carboxypeptidase.
SQ
Query Match 35.9%; Score 1539; DB 11; Length 353;
Best Local Similarity 81.2%; Pred. No. 1.5e-105;
Matches 285; Conservative 22; Mismatches 44; Indels 0; Gaps 0;
Qy 1 MSSSSWLLLSLVAVTAQAQSTIEQAKTFLDKFNHEADLFYQSSLASWNTNITENVQ 60
Db 1 MSSSSWLLLSLVAVTAQAQSTIEQAKTFLDNFNQEAEDLSYQSSLASWNTNITENNAQ 60
Qy 61 MNVAGDKWSAFLKEQSTLAQMYFLOEIQNTLVKQLQALQQGSSVLSSEDKSKRLNTIL 120
Db 61 KMSEAAAKWSAFYEQSKTAQSFSLQIQTPITIKRQLQALQQGSSALSADKKNQLNTIL 120
Qy 121 NTMTSTIYSTGKVCNPDNPQECCLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLY 180
Db 121 NTMTSTIYSTGKVCNPKPKPQECCLLEPGLDEIMATSTDYNSRLWAWESWRAEVGKQLRPLY 180
Qy 181 EBYVVLKEMARAHYEDYDGYWGDYEVNGVDGYDSRGQLIEDVHTFEEIKPLYEHL 240
Db 181 EBYVVLKEMARAHYEDYDGYWGDYEVNGVDGYDSRGQLIEDVHTFEEIKPLYEHL 240
Qy 241 HAYVRKLMNAYPSVISPIGCLPAHLGDMWGRFTWNLVSLTVPFGQKPNIDVTDMVQ 300
Db 241 HAYVRKLMNAYPSVISPIGCLPAHLGDMWGRFTWNLVSLTVPFGQKPNIDVTDMVQ 300
Qy 301 AWDQRIKFAEKFPVSVGLNPMWQGFENSMITDPCGVQKAVCHPTAWDL 351
Db 301 GWDARIFQEAKEKFPVSVGLNPMWQGFENSMITDPCGVQKAVCHPTAWDL 351
RESULT 7
QBN710 PRELIMINARY; PRT; 739 AA.
AC QBN710;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to angiotensin I converting enzyme (Peptidyl-dipeptidase A)
DE 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RA Strausberg R.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC036375; AAH36375.1; -.
DR InterPro; IPR001548; Peptidase_M2.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; PEPDIPASEA.
DR PRODOM; PD004184; Peptidase_M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ
Query Match 31.4%; Score 1347.5; DB 4; Length 739;
Best Local Similarity 40.4%; Pred. No. 6.7e-91;
Matches 266; Conservative 125; Mismatches 224; Indels 43; Gaps 12;
Qy 16 AAQS---TIEQAKTFLDKFNHEADLFYQSSLASWNTNITTEE-----NVQNMN 63
Db 62 SAQSPNLTDEAEASKFVEEDRTSQVWNEYAEANWNTNITETSKILLQKNQMOIAN 121
Qy 64 NAGDKWSAFLKEQSTLAQMYFLOEIQNTLVKQLQALQQGSSVLSSEDKSKRLNTILTM 123
Db 122 HT-----LKYGTQARKFDVNQLONTTIKRIIKVQDLERAALPAQEEYKRLDM 173
Qy 124 STIYSTGKVCNPDNPQECCLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEY 183
Db 174 ETTYSVATVCHPNG--SCLEPDLTNWATSRKYEDLLWAGWGRDKAGRAILOFYPKY 231
Qy 184 VVLKEMARAHYEDYDGYWGDYEVNGVDGYDSRGQLIEDVHTFEEIKPLYEHLHAY 243
Db 232 VELINQAARLNGYVDAGDSWRSMYETPSLE-----QDLERLFOELQFLYINLHAY 281
Qy 244 VRKLMNAY-PSYISPIGCLPAHLGDMWGRFTWNLVSLTVPFGQKPNIDVTDMVQDAW 302
Db 282 VRALRHRYGAOHINLEGPVPAHLGDMWGRFTWNLVSLTVPFGQKPNIDVTDMVQDAW 341
Qy 303 DAQRIKFAEKFPVSVGLNPMWQGFENSMITDPCGVQKAVCHPTAWDLGKG-DPRILMC 361
Db 342 TPRRMKEADDFTSGLLPPVPEFNKSMLEKPTDGRVTVCHASAWDFYNGKDFRIKQC 401
Qy 362 TKVTWDDFLTAHENGHTQYDMAYAAQFLLRNGNNEGFHEAVGEINLSAATPKHLKSI 421
Db 402 TTVNLEDLVVAHENGHTQYDMAYAAQFLLRNGNNEGFHEAVGEINLSAATPKHLKSI 461
Qy 422 GLISPDFQEDNDETEINFLKQALITVGLTPFTYMLEKRWVVFKEIPKQDMKKWEMK 481
Db 462 NLLSSEGGSD-EHDINFLMKVAKLDKAFIPFSYLVQWQWRVFDGSIKENTNQESWLSR 520
Qy 482 REIVGVVPEVPHDETICDPAFLFHVSNYSFIRYTRLYQFQFOEALCOAKHEGPLHK 541
Db 521 LKYQGLCPVPPTQDFDPGAKFHPSSVPYIRYFVSPFIQFQFHEALCOAGHTGPLHK 580
Qy 542 CDISNSTAGOKLFNMLRLGKSEPTLALENVVGAKNMVRPLNLYFFPFLFTWLDQNK- 600
Db 581 CDLYQSKAGORLATAMKLGSRPWPPEAMQLITGPNWSASAMLSYKFKPLDLWLTENEL 640
Qy 601 -NSFVGW-STDWSPVAD---QSIKVRISLKGALGKAYEWNDNENMYLFSSVAYAMRQ 653
Db 641 HGEKLGWPOYNWTPNSDDFYNETETKFIQ--FYDQTGIWDHGAHLLPSPQARGTRE 696
RESULT 8
Q9GLN6 PRELIMINARY; PRT; 732 AA.
ID Q9GLN6;
AC Q9GLN6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Dipeptidyl carboxy peptidase 1 testicular form.
DE DCPI.
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OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20469400; PubMed=11013071;
 RA Dufour C., Casane D., Denton D., Wickings J., Corvol P.,
 RA "Human-Chimpanzee DNA sequence variation in the four major genes of
 RT the renin angiotensin system";
 RL Genomics 69:14-26(2000).
 DR EMBL; AF193476; AAG31359.1; JOINED.
 DR EMBL; AF193477; AAG31359.1; JOINED.
 DR EMBL; AF193478; AAG31359.1; JOINED.
 DR EMBL; AF193479; AAG31359.1; JOINED.
 DR EMBL; AF193480; AAG31359.1; JOINED.
 DR EMBL; AF193481; AAG31359.1; JOINED.
 DR EMBL; AF193482; AAG31359.1; JOINED.
 DR EMBL; AF193483; AAG31359.1; JOINED.
 DR EMBL; AF193484; AAG31359.1; JOINED.
 DR EMBL; AF193485; AAG31359.1; JOINED.
 DR InterPro; IPR001548; Peptidase M2.
 DR PRINTS; PR00791; PEPTIDASEA.
 DR ProDom; PD004184; Peptidase M2; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR SEQUENCE 732 AA; 83428 MW; C43D06443A47E74B CRC64;
 Query Match 31.1%; Score 1336; DB 6; Length 732;
 Best Local Similarity 41.6%; Pred. No. 4.7e-90;
 Matches 256; Conservative 119; Mismatches 205; Indels 38; Gaps 10;
 QY 15 TAAQS-----TIEQAKTFLDKFNHEAEDLFYOSSLASWYNTNITE-----NVQNM 62
 DB 61 TSAQSNLTDBAASKFVEEDRTSQVWVEAYEANNWYNTNITETSKILLQNMQIA 120
 QY 63 NNAGDKWSAFLKEQSTLAQMYPIORIONLTVKLQALQONGSSVLSDEKSKRLNTI 122
 DB 121 NHT-----UKYQOARRFDVQNLQNTTIKRIKKVQDLERAAIPQAEIEYNKILLD 172
 QY 123 MSTYTGKVCNPDNPQECILLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 182
 DB 173 METTYSVATVCHTG--SCLQLEPDLTNWATSRKYEDLLWAWEGWDRKAGRAILQFYPK 230
 QY 183 YVVLKNEMARANYEDYGDYWRGDIYVNGDYGVSRSGLIEDVHTFEEIKPLVYELHA 242
 DB 231 YVELINQOARLNGYVDAGDSWRSMTETPSLE-----QDLERLFOELQPLVYLHA 280
 QY 243 YVRKALMNAV-PSYISPIGCLPAHLGDMWGRFWNTNLSLTVPFGQKPNIDVTDAVDQA 301
 DB 281 YVRALHRYGACHINLEGPFAHLGNMAQWTSNIYDLVVPFSPASMD*TEAMLKQG 340
 QY 302 WDQRIKFEAKFVSVGLPNMTQGWENSMITDPCGNOKAVCHPTAWDLGK--DPRILM 360
 DB 341 WTPRRMFKEADDFTSGLGLFVPEPFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQ 400
 QY 361 CTKVTVDDFTTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHAEGEIMSLAATPKHLKS 420
 DB 401 CTTVNLDELVAHHEMGHIQYFMOYKDLPAVALREGANPGFHAIGDVLALSYSTPKHLHS 460
 QY 421 IGLLSPDFQEDNETENFLKQALTTVGLTPFTYMLEKRWMMVFKEIPIKQDMKKWEM 480
 DB 461 LNLSSGGSD-EHDINFLMKALDKIAFIPFSYLVDMWRVFDGSIITKENYNQEWMSL 519
 QY 481 KREIVGVVEVPDHEITYCDPASLHFVSNDSYFRTYRTLYOFQFOALCQAQKHEGPLH 540
 DB 520 RLKQGLCPVPRTQGFDFDCAKEHIPSSVPIRYFVFSIIQFQFHEALCQAAGHTGPLH 579

QY 541 KCDISNSTEAGOKLFNMRLRGKSEPTWLTALENVVCAKMNVRPLNLYEPELFTWLKDONK 600
 DB 580 KCDIYQSKEAGQRLATAMKLGFSRWPPEAMQLITQPPNNSASAMLSYFKPLDMLWTRENE 639
 QY 601 --NSFWG--STDWSPYADQS 617
 DB 640 LHGEKLGWPQYNWTPNSARS 659
 RESULT 9
 Q8K233 PRELIMINARY; PRT; 1015 AA.
 ID Q8K233
 AC Q8K233
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ACE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC034367; AAH34367.1; -.
 DR MGD; MGI:87874; Ace.
 DR InterPro; IPR001548; Peptidase M2.
 DR InterPro; IPR006025; Zn_MTPeptase.
 DR Pfam; PF01401; Peptidase M2; 2.
 DR PRINTS; PR00791; PEPTIDASEA.
 DR ProDom; PD004184; Peptidase M2; 2.
 DR PROSITE; PS00142; ZINC_PROTEASE; 2.
 DR Hypothetical protein.
 FT NON TER
 KW NON TER
 SQ SEQUENCE 1015 AA; 117509 MW; D097F69585553C27 CRC64;
 Query Match 31.1%; Score 1334; DB 11; Length 1015;
 Best Local Similarity 42.6%; Pred. No. 1.1e-89;
 Matches 255; Conservative 112; Mismatches 213; Indels 18; Gaps 7;
 QY 20 TIEQAKTFLDKFNHEAEDLFYOSSLASWYNTNITEVQNNNAGDKWSAFLKEQSTL 79
 DB 415 TDAKADRFVEEDRTAQVLLNEAYEANNWYNTNITEGSKILLEKSTEVNHTLVGTR 474
 QY 80 AQMYPLQEIQLNLTVKLQALQONGSSVLSDEKSKRLNTIILNTMTIYTGKVCNPDNPQ 139
 DB 475 AKTFDVSNFQNSIKRIKKIKNLDRVLPPEKEEYNQILLDMETYSLSNICYTNG-- 532
 QY 140 ECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEYVVLKNEMARANYEDY 199
 DB 533 TCMPLPDLTNWATSRKYEELLWAWESWRDKVGRAILPPFPKYVFSNKIAXLNGYTD 592
 QY 200 GDYWRGDIYVNGDYGVSRSGLIEDVHTFEEIKPLVYELHAHAYRAKLMNAPYS-YISP 258
 DB 593 GDSNRSLYESDNLE-----QDLEKLYQELQPLVNLHAYVRSRSLRHHYGSYINL 642
 QY 259 IGCLPAHLGDMWGRFWNTNLSLTVPFGQKPNIDVTDAVDQAWDAQRIKFEAKFVSV 318
 DB 643 DGPIPAHLGNMAQWTSNIYDLVAPFSPAPNIDATEAMIKQGTWPRIFKEADNFTSL 702
 QY 319 GLPNMTQGFWENSMITDPCGNOKAVCHPTAWDLGK--DPRILMCTKVTVDDFTTAHHEMG 377
 DB 703 GLLPVPEPFWNKSMLEKPTDGREVVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHEMG 762
 QY 378 HIQYDMAYAAQPFLLRNGANEGFHAEGEIMSLAATPKHLKSIGLLSPDFQEDNETEIN 437
 DB 763 HIQYFMQKLPVTFREGANPGFHAIGDINLALSVSTPKELYSINLSTE-GSGYEVDIN 821
 QY 438 FLLKQALTTVGLTPFTYMLEKRWMMVFKEIPIKQDMKKWEMKREIVGVVEVPDHEITY 497

QY 80 AQMPYLOEIQNTLVKQLQALQONGSSVLSSEKSKRLNTILNTMTSTYSTGKVCNPNQ 139
 DB 172 AKTFVNFQNSTIKRIIKVQNVDRVLPENEESEYNQILLMETTYSVANVCYTG-- 229
 QY 140 ECLLEPGLNEIMANSLDYNERLWAKESRSEVGHQALPPLYEEVVLKNEMARANHYEDY 199
 DB 230 TCLSLEPDLTNIMATSRKYEEELLWVWKSMDKVGRAILPFPKYVDFSNKIACLNGYSDA 289
 QY 200 GDYWRGDYVNGVDGYDSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP 258
 DB 290 GDSWRSSYSDLE-----QDEKLYQELQPLYLNLHAYVRRSLHRHYSYINL 339
 QY 259 IGCPLPAHLGDMWGRFWTNLYSLTVPGOKNIDVTDAMVDOANDAOIRIPEAKFPFVS 318
 DB 340 DGPPIPAHLGDMWAGTWSNIYDLVAPFAPSIDATEAMI KOGWTPRRIPEAKDNFTSL 399
 QY 319 GLPNMTQGFWNSMLTDPGNVQKAVCHPTAMD LGK-DPRILMCTKVTDMDFLTAHEMG 377
 DB 400 GLLPVPEPFWNSMLKPTDGRVNVCHASAWDFYNGKDFRIKQCTSVNMEELVIAHEMG 459
 QY 378 HIQYDWAYAAQPFLLRNGANEGFHEAVGEIMSLAATPKHLKSLIGLSPOFQEDNETEIN 437
 DB 460 HIQYFQYKDLPTVTFREGANPGFHEAIGDVLALSSTPKHLHSLNLSSE-GSGYEHIN 518
 QY 438 FLKQALATVGTLPFTYMLKRWVFKGEIPKQDMKMKWEMKREIVGVVPEVPHDET 497
 DB 519 FLKQALDIAFIPIPSYLIIDQWRVFDGSIKENYQEWMSLRLKYQGLCPPVPRSQGD 578
 QY 498 CPASLPHVSNDSYPIRYTRTYLQFOFQALCOAKHEGLPKCDISNSTEAGKLFNM 557
 DB 579 FPGSKFHPVNPVIRFISFIIOFQHEALCRAAGHTGPLYKCDIYQSKAGKLLADA 638
 QY 558 LRLGKSEPTWLALENVVGAKNNVRLNLYPEPLFTWLKQDNK--NSFVGW-STDWSP 612
 DB 639 MKLGYSKQWPEAMKIITQPNMSASAIMNYFKPLTEWLVTENRHRTGLWPEYTWTP 696

RESULT 12
 Q9EQM9 PRELIMINARY; PRT; 1313 AA.
 ID Q9EQM9
 AC Q9EQM9, 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Angiotensin-converting enzyme.
 GN ACE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NCBI_TaxID=10116;
 RN [1] --
 RP SEQUENCE FROM N.A.
 RC STRAIN=F344/N; TISSUE=Lung;
 RA Jafarian-Tehrani M., Listwak S., Barrientos R.M., Michaud A.,
 RA Corvol P., Sternberg E.M.;
 RT "Characterization of a missense mutation in the angiotensin I-
 RT converting enzyme cDNA in exudative inflammation resistant F344/N
 rats";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF201331; AAC35596.1; --
 DR InterPro; IPR001548; Peptidase M2.
 DR InterPro; IPR006025; Zn.MTpeptidase.
 DR Pfam; PF01401; Peptidase M2; 2.
 DR PRINTS; PR00791; PEPTIDASEA.
 DR PRODOM; PD004184; Peptidase M2; 2.
 DR PROSITE; PS00142; ZINC_PROTEASE; 2.
 SQ SEQUENCE 1313 AA; 150941 MW; 5888341562542804 CRC64;

Query Match 30.5%; Score 1310; DB 11; Length 1313;
 Best Local Similarity 42.0%; Pred. No. 9.3e-88;
 Matches 251; Conservative 115; Mismatches 214; Indels 18; Gaps 7;
 QY 20 TIEQAKTFLDKENHAEADLFVQSSLASWNTNTIENVQNMNAGDKSAFLKEQSTL 79

DB 650 TDEAKANFVEEYDRTAKVLWNEVAEANYNTNITIEGSKILLQKNKEVSNHLYGTW 709
 QY 80 AQMPYLOEIQNTLVKQLQALQONGSSVLSSEKSKRLNTILNTMTSTYSTGKVCNPNQ 139
 DB 710 AKTFVNFQNSTIKRIIKVQNVDRVLPENEESEYNQILLMETTYSVANVCYTG-- 767
 QY 140 ECLLEPGLNEIMANSLDYNERLWAKESRSEVGHQALPPLYEEVVLKNEMARANHYEDY 199
 DB 768 TCLSLEPDLTNIMATSRKYEEELLWVWKSMDKVGRAILPFPKYVDFSNKIACLNGYSDA 827
 QY 200 GDYWRGDYVNGVDGYDSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP 258
 DB 828 GDSWRSSYSDLE-----QDEKLYQELQPLYLNLHAYVRRSLHRHYSYINL 877
 QY 259 IGCPLPAHLGDMWGRFWTNLYSLTVPGOKNIDVTDAMVDOANDAOIRIPEAKFPFVS 318
 DB 878 DGPPIPAHLGDMWAGTWSNIYDLVAPFAPSIDATEAMI KOGWTPRRIPEAKDNFTSL 937
 QY 319 GLPNMTQGFWNSMLTDPGNVQKAVCHPTAMD LGK-DPRILMCTKVTDMDFLTAHEMG 377
 DB 938 GLLPVPEPFWNSMLKPTDGRVNVCHASAWDFYNGKDFRIKQCTSVNMEELVIAHEMG 997
 QY 378 HIQYDWAYAAQPFLLRNGANEGFHEAVGEIMSLAATPKHLKSLIGLSPOFQEDNETEIN 437
 DB 998 HIQYFQYKDLPTVTFREGANPGFHEAIGDVLALSSTPKHLHSLNLSSE-GSGYEHIN 1056
 QY 438 FLKQALATVGTLPFTYMLKRWVFKGEIPKQDMKMKWEMKREIVGVVPEVPHDET 497
 DB 1057 FLKQALDIAFIPIPSYLIIDQWRVFDGSIKENYQEWMSLRLKYQGLCPPVPRSQGD 1116
 QY 498 CPASLPHVSNDSYPIRYTRTYLQFOFQALCOAKHEGLPKCDISNSTEAGKLFNM 557
 DB 1117 FPGSKFHPVNPVIRFISFIIOFQHEALCRAAGHTGPLYKCDIYQSKAGKLLADA 1176
 QY 558 LRLGKSEPTWLALENVVGAKNNVRLNLYPEPLFTWLKQDNK--NSFVGW-STDWSP 612
 DB 1177 MKLGYSKQWPEAMKIITQPNMSASAIMNYFKPLTEWLVTENRHRTGLWPEYTWTP 1234

RESULT 13
 Q15540 PRELIMINARY; PRT; 694 AA.
 ID Q15540
 AC Q15540, 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE DCPI protein.
 GN DCPI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1] --
 RP SEQUENCE FROM N.A.
 RC MEDLINE=90046671; PubMed=2554286;
 RA Ehlers M.R., Fox E.A., Strydom D.J., Riordan J.F.;
 RT "Molecular cloning of human testicular angiotensin-converting enzyme:
 RT the testis isozyme is identical to the C-terminal half of endothelial
 RT angiotensin-converting enzyme.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:7741-7745 (1989).
 DR EMBL; M26658; AAA60612.1; --
 DR InterPro; IPR001548; Peptidase M2.
 DR InterPro; IPR006025; Zn.MTpeptidase.
 DR Pfam; PF01401; Peptidase M2; 1.
 DR PRINTS; PR00791; PEPTIDASEA.
 DR PRODOM; PD004184; Peptidase M2; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 SQ SEQUENCE 694 AA; 79333 MW; 57C0FF9C5AEC119 CRC64;

Query Match 30.4%; Score 1303; DB 4; Length 694;
 Best Local Similarity 42.7%; Pred. No. 1.2e-87;
 Matches 250; Conservative 107; Mismatches 195; Indels 34; Gaps 9;


```
RL Insect Biochem. Mol. Biol. 31:97-103 (2001).
DR EMBL: AB026110; BAA97657.1; -.
DR MERO89: M02.002; -.
DR InterPro: IPR001548; Peptidase_M2.
DR InterPro: IPR006025; Zn_MTPeptide.
DR Pfam: PF01401; Peptidase_M2; 1.
DR PRINTS: PR00791; PEPTIDASEA.
DR ProDom: PD004184; Peptidase_M2; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 648 AA; 74917 MW; 9A740AA9FCACEBF0 CRC64;

Query Match      25.48; Score 1089.5; DB 5; Length 648;
Best Local Similarity 35.6%; Pred. No. 6.7e-72;
Matches 232; Conservative 125; Mismatches 259; Indels 35; Gaps 11;

QY 11 LVAVTAQSTIEQAK-TFLDKNFHEADLFY-----OSSLASKNYNTNTEEN 58
DB 10 LJAIAVAVFIVATQGRDPDLEAREHEAREYMLHLDKATGLRKNRASLAWEYTSNITKEN 69
QY 59 VQNNNAGDKWSAFLEKQSTLAQMYPLQETQNTLVKLQALQOQNGSSVLSEDKSKELNT 118
DB 70 EEKSIQTHLELSRQEKAAWETKMYGQDFDFTLRMFKKYSQLGVAALPDDKFAALMR 129
QY 119 ILNTMSTIYTGKVCNPDNPOEC-LLLEPGLNEITMANSLDYNBELMAWESRSEVGKOLR 177
DB 130 TVSGMESNYATAKICSYKNESKCDLSLEPEITEIFSTQDPPEELKHAWEVHNAAGATAK 189
QY 178 PLYEYVVLKEMARAHYEDYDWRGDYVNGDGYDSRGOLIEDVEHTEEEKPLY 237
DB 190 KNFTDYVNLNEAAKNGFDNVAEWQSEYEVDPFE-----EQLAKLWEDVAPLY 239
QY 238 EHLHAYVRAKLMNAY-PSYISPIGCLPAHLGLDMWGRFWTNLYSLTVPFGOKPNIDVTD 296
DB 240 QQLHAYVKRLRDYKGVKVSARGPIPAHLGLGNWQAQTWNIESFTRPYDPKKEIDVTOA 299
QY 297 MVDQAWDAQRIPEKAEKFFVUGLENMTQGTWENSMLTDPGNVOKAYCHPTAMDLGK-D 355
DB 300 MRDQNYTPMKMFQMSDEFPSLNTAMPEKFWKNSIIEKPTD-REIVCHASANDFFDGED 358
QY 356 PRILMCTKVTDDELTAHEHMGHICYDMAYAAQPELLRNGANEGFHEAVGEINSLSAATP 415
DB 359 FRIKQCTTVDYEFYQTTHMGHICYYLYQYRDQPVVFDGANGQGFHEAVGDTIALSVSSP 418
QY 416 KHLKSGILSPDFQEDNTEINFLKQALTIVGTLPFTYMLEKWRWVFKGEIEPDQWVK 475
DB 419 KHLRVGLATGD-AEDEQTEINQLYKMGIDKIAFLPFAYTLDLFRYGVFREKTLPEIDYNC 477
QY 476 KWEKREIVGVVEVPVPHDETYCDPASLFHVSNDYSPIRYVTRTYQFQFOEALCO-AAK 534
DB 478 HYWKUREQQGVVEPPVNRTEDDFDAAKYHVSNSVVEYARYVVSFIQFHRGVQCLAGE 537
QY 535 HEG-----PLHKCDISNSTEAGOKLFNMLRLGKSEFWTLALENVVGAKNMVRPLINYPE 589
DB 538 HAAGDPNKKLVDCDIYQSVAAAGNALANMLKMGSSKFPDAMEALTQGREMKADGLLEYFR 597
QY 590 PLFTWLKDQKNKS--FVGHSTDSVPYADQSIKVRISLKSALGDKAYEWNND 638
DB 598 PLHDWLRAENQRTGEHIGWEPNTMEYCTPSQLSELNVKEPSSPATQOSDS 648
```

Search completed: February 19, 2004, 19:51:08
Job time : 45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 19, 2004, 19:47:53 ; Search time 21 Seconds
(without alignments)
3686.466 Million cell updates/sec

Title: US-09-163-648-2

Perfect score: 4291

Sequence: 1 MSSSSMLLSLVAVTAQAQT.....ISKGNNPGFQNTDDVQTGF 805

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76:*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	4281	99.8	804	T14762	hypothetical prote
2	1344	31.3	732	S05238	peptidyl-di-peptida
3	1337	31.2	1306	A31759	peptidyl-di-peptida
4	1334	31.1	732	A35655	peptidyl-di-peptida
5	1334	31.1	1312	A34171	peptidyl-di-peptida
6	1312	30.6	1193	JC2489	peptidyl-di-peptida
7	1310	30.5	1313	JC2038	peptidyl-di-peptida
8	1283	29.9	737	A34402	peptidyl-di-peptida
9	1283	29.9	1309	S35484	peptidyl-di-peptida
10	1058	24.7	611	S65472	peptidyl-di-peptida
11	1039	24.2	615	A57533	peptidyl-di-peptida
12	1030	24.0	630	JC5374	angiotensin-conver
13	642.5	15.0	907	T15792	hypothetical prote
14	157	3.7	532	C83696	hypothetical prote
15	154	3.6	502	AFL1310	probable thermosta
16	147	3.4	502	A21682	probable thermosta
17	139.5	3.3	987	A12011	peptide synthetase
18	139	3.2	608	B82938	zinc metalloprotei
19	136	3.2	611	D82881	zinc metalloprotei
20	135	3.1	501	D69943	carboxypeptidase h
21	125	2.9	627	A40048	1,4-alpha-glucan b
22	124.5	2.9	987	I40373	G-utrophin - mouse
23	124	2.9	538	E72561	probable thermosta
24	123.5	2.9	902	E90270	conserved hypotet
25	123	2.9	990	E23416	lactibiotic epider
26	122	2.8	642	E98000	1,4-alpha-glucan b
27	121	2.8	607	AB3511	oligodeopeptidase
28	121	2.8	1034	T30574	beta-galactosidase
29	120	2.8	1339	A84683	probable SNF2 subf

RESULT 1

T14762

hypothetical protein DKFp434A014.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T14762

R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, August 1999

A:Reference number: Z18181

A:Accession: T14762

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-804 <WAM>

A:Cross-references: EMBL:AL110224

A:Experimental source: adult testis; clone DKFp434A014

C:Genetics:

A:Ncte: DKFp434A014.1

Query Match 99.8%; Score 4281; DB 2; Length 804;

Best Local Similarity 99.9%; Pred. No. 6.9e-288;

Matches 803; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	2	SSSSMLLSLVAVTAQAQTIEQAKTFLDKFNHEADLFYQSSLASWYNNTNTEENVON	61
DB	1	SSSSMLLSLVAVTAHAHSTIEEQAKTFLDKFNHEADLFYQSSLASWYNNTNTEENVON	60
QY	62	MNAGDKWSAFLEKEOSTLAQMTPLQEIQLNLTVKLQALQONGSSVLSEDKSKRLNTILN	121
DB	61	MNAGDKWSAFLEKEOSTLAQMTPLQEIQLNLTVKLQALQONGSSVLSEDKSKRLNTILN	120
QY	122	TWSTIYSTGKVCNPNPQECILLLEPGLNEIMANSLDYNERLWAWESWSEVKQRLPIYE	181
DB	121	TWSTIYSTGKVCNPNPQECILLLEPGLNEIMANSLDYNERLWAWESWSEVKQRLPIYE	180
QY	182	EYVLKNEVARANHYEDYDVRGVDYNGVDYSGQLIEDVHEFTFEELKPYEHLH	241
DB	181	EYVLKNEVARANHYEDYDVRGVDYNGVDYSGQLIEDVHEFTFEELKPYEHLH	240
QY	242	AYVRKIMNAPSYISPIGCLPAHLIGDMWGSFWTNLYSLTVPPFGQKNIDVTDAMVQA	301
DB	241	AYVRKIMNAPSYISPIGCLPAHLIGDMWGSFWTNLYSLTVPPFGQKNIDVTDAMVQA	300
QY	302	WDAQRFKEAEKFFVSGVLPNNMTQGFWNSMLTDPNQKAVCHPTAMDGLGKDFRILMC	361
DB	301	WDAQRFKEAEKFFVSGVLPNNMTQGFWNSMLTDPNQKAVCHPTAMDGLGKDFRILMC	360
QY	362	TKVTMDDFLTAFHEMGHIQYDMAYAAQPELLRNGANEGFHEAVGEIMSLSAATPKHLKSI	421
DB	361	TKVTMDDFLTAFHEMGHIQYDMAYAAQPELLRNGANEGFHEAVGEIMSLSAATPKHLKSI	420
QY	422	GLLSPPFQEDNETEINFLIKQALTIYGTLPFTVMLEKRWVFKGEIPKQDNKKWENK	481

30	119.5	2.8	1283	2	S52500	oxysterol-binding
31	119.5	2.8	3655	2	T38084	TRAP-like protein
32	119.5	2.8	4540	2	T30838	cytoplasmic dynein
33	118.5	2.8	1780	2	T17272	hypothetical prote
34	118	2.7	642	2	G95129	1,4-alpha-glucan b
35	117	2.7	1575	2	G82905	conserved hypotet
36	116	2.7	963	2	C90535	conserved hypotet
37	116	2.7	1642	2	T08880	NMDA receptor-bind
38	116	2.7	1939	2	D97316	probable S-layer p
39	115.5	2.7	611	2	A75573	probable oligoendo
40	115.5	2.7	3433	1	S28381	utrophin - human
41	115	2.7	524	2	B82202	thermostable carbo
42	115	2.7	950	2	A71655	hypothetical prote
43	115	2.7	952	2	T50431	hypothetical coile
44	114.5	2.7	901	2	A48653	phage infection pr
45	114.5	2.7	1225	1	B64234	hypothetical prote

Db 421 GLLSPDFQEDNETETINFLKQALITVGTLPFTYMLEKWRWVFKGEITPKDQWKKWEMK 480
QY 482 REIVGVVPEVPHDEYCDPASLFHVSNDYSFIRYVTRILYQFOFOEALCOAKHEGPHLK 541
Db 481 REIVGVVPEVPHDEYCDPASLFHVSNDYSFIRYVTRILYQFOFOEALCOAKHEGPHLK 540
QY 542 CDISNSTEAGOKLFNMLRGKSEPTWLALENVVGAKNNVRLPLNYPPEFTLWLDQKN 601
Db 541 CDISNSTEAGOKLFNMLRGKSEPTWLALENVVGAKNNVRLPLNYPPEFTLWLDQKN 600
QY 602 SFVGSWSTWSPVADOSIKVIRISLKSALGDKAYEWNDNEMYLFRSSVAYAMQYFLKVKQ 661
Db 601 SFVGSWSTWSPVADOSIKVIRISLKSALGDKAYEWNDNEMYLFRSSVAYAMQYFLKVKQ 660
QY 662 MILFGEEDVRVANLKRISFNFFVAPKNVSDIIIRTEVEKAIKRSRINDAFRLNDS 721
Db 661 MILFGEEDVRVANLKRISFNFFVAPKNVSDIIIRTEVEKAIKRSRINDAFRLNDS 720
QY 722 LEFLGIQPTLGPNNQPPVSIWLVFGVVGVIWVGIVILIFGTIRDRKKKNKARSGENPY 781
Db 721 LEFLGIQPTLGPNNQPPVSIWLVFGVVGVIWVGIVILIFGTIRDRKKKNKARSGENPY 780
QY 782 ASDISKGNNGFQNTDDVQTSF 805
Db 781 ASDISKGNNGFQNTDDVQTSF 804

RESULT 2
S05238
peptidyl-di-peptidase A (EC 3.4.15.1) precursor, testicular splice form - human
N:Alternate names: angiotensin I-converting enzyme (ACE); CD143; dipeptidyl carboxypeptidase
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 02-Jul-1998 #text_change 18-Jun-1999
C:Accession: S05238; A33979
R:Lattion, A.L.; Soubrier, F.; Allegri, J.; Hubert, C.; Corvol, P.; Alhenc-Gelas, F.
FEBS Lett. 252, 99-104, 1989
A:Title: The testicular transcript of the angiotensin I-converting enzyme encodes for the
A:Reference number: S05238; MUID:89338720; PMID:2547653
A:Accession: S05238
A:Molecule type: mRNA
A:Residues: 1-732 <EHL>
A:Cross-references: EMBL:X16295; NID:g28264; PIDN:CAA34362.1; PID:g28265
R:Enlars, M.R.W.; Fox, E.A.; Strydom, D.J.; Riordan, J.F.
Proc. Natl. Acad. Sci. U.S.A. 86, 7741-7745, 1989
A:Title: Molecular cloning of human testicular angiotensin-converting enzyme: the testis
A:Reference number: A33979; MUID:90046671; PMID:2554286
A:Accession: A33979
A:Molecule type: mRNA
A:Residues: 1-732 <EHL>
A:Cross-references: GB:M26657; NID:g338666; PIDN:AAA60611.1; PID:g338667
A:Experimental source: clones R1.2 and T8B
A:Note: neither the complete nucleic acid sequence nor the complete translation are shown
C:Comment: For the renal and pulmonary splice form, see PIR:A31759.
C:Genetics:
A:Gene: GDB:DCPI; ACE
A:Cross-references: GDB:119840; OMIM:106180
A:Map position: 17q23-17q23
C:Function:
A:Description: catalyzes the hydrolysis of dipeptides from the carboxyl end of polypeptide
C:Superfamily: mammalian peptidyl-di-peptidase A
C:Keywords: alternative splicing; glycoprotein; metalloproteinase; peptidyl dipeptide hydrolase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-732/Product: peptidyl dipeptidase I #status predicted <MAT>
F:686-702/Domain: transmembrane #status predicted <TRM>
F:103,121,140,186,368,617,651/Binding site: carboxylate (Asn) (covalent) #status predicted
F:414,418,434/Binding site: zinc, catalytic (His, His, Glu) #status predicted
F:415/Active site: Glu #status predicted

Query Match 31.3%; Score 1344; DB 1; Length 732;
Best Local Similarity 41.8%; Pred. No. 7.7e-85;
Matches 259; Conservative 119; Mismatches 204; Indels 38; Gaps 10;

QY 15 TAAQS-----TIEQAKTFLDKFNHEADLFYQSSLASWNTNITEE-----NVQNM 62

Db 61 TSAQSNLVTDEAEASKFVEEYDRTSQVVMNYSAAENMNTNITETSKILLQKMQIA 120
QY 63 NNAAGDKWSAFLKEOSTLAQWYPLQEIQLNTVTKLQALQONGSSVLSLDSKRLNTILNT 122
Db 121 NHT-----LKYGTQARKFDVNLQNTTKRIKKVQDLERAAALPAQELBEYNNKILLD 172
QY 123 MSTIYGTGKVCNPDNPQECILLLEPGLINEIMANSLDYNELNMAWESRWSRSGVQLAPLVEE 182
Db 173 METTYSVATVCHPNG--SCLQLEPDLTNMATSRYKEDLLNAWEGWRDAGARAILQFYFPR 230
QY 183 YVVLKVMENAPANHYEDYDWRGDEVNGVDGYDSRGQLIEDVHTFEIIPKLYEHLHA 242
Db 231 YVELINQAALNGYVDAGDSRWSMYETPSLE-----QDLERLPQELQPLYNLHA 280
QY 243 YVRAKLNNAY-PSYISPIGCLPAHLGLDMGAFWNTNLYSLTVPFQKPNIDVTDMVDQA 301
Db 281 YVRALHRYGAHINLEGP1PAHLGLGNMAQTNISYDLVVPFPPSAPSMOTTEAMLKOG 340
QY 302 WDAORIFKAEKFFSVGLPNMTQGFWENSLMDPGNVQKAVCHPTAWDLGKG-DPRILM 360
Db 341 WTPRRMFKAADFTSLGLLPVPEPFNWKSMLEKPTDGREVVCHASANDFYNGKDFRIQ 400
QY 361 CTKVMTDDFLTAHHEMCHIQYDMAYAAQPFLLRNGANEGFHEAVGIMSLSAATPKHLKS 420
Db 401 CTTVNLDELVAHHEMCHIYFMQYKDLPLVALREGANPGFHEAIGDVLALSVPKHLHS 460
QY 421 IGLSPDFQEDNETETINFLKQALITVGTLPFTYMLEKWRWVFKGEITPKDQWKKWEM 480
Db 461 INLLSSGGSD-EHDINFLMKALDKIATIPFSYLVQDWRVFDGSIITKENYNQEWNSL 519
QY 481 KREIVGVVPEVPHDEYCDPASLFHVSNDYSFIRYVTRILYQFOFOEALCOAKHEGPHLK 540
Db 520 RLKYQGLCPVPRTQGDFFDGAKEFHIPSSVPYIRYFVFIQPFQHEALCOAAHGTPHLH 579
QY 541 KCDISNSTEAGOKLFNMLRGKSEPTWLALENVVGAKNNVRLPLNYPPEFTLWLDQKN 600
Db 580 KCDIYQSKRAGQRLATMLKGFSPRPFAEMQLITGQPNWSASAMLSYFRLDLDLRTENE 639
QY 601 --NSFVGW-STDWSPYADQS 617
Db 640 LHGEKLGMPQVNTWTFNSARS 659

RESULT 3
A31759
peptidyl-di-peptidase A (EC 3.4.15.1) precursor, renal and pulmonary splice form - human
N:Alternate names: angiotensin I-converting enzyme (ACE); CD143; dipeptidyl carboxypeptidase
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1990 #sequence_revision 02-Jul-1998 #text_change 18-Jun-1999
C:Accession: A31759; PQ0004
R:Soubrier, F.; Alhenc-Gelas, F.; Hubert, C.; Allegri, J.; John, M.; Tregear, G.; Corvol, P.
Proc. Natl. Acad. Sci. U.S.A. 85, 9386-9390, 1988
A:Title: Two putative active centers in human angiotensin I-converting enzyme revealed
A:Reference number: A31759; MUID:89071703; PMID:2849100
A:Accession: A31759
A:Molecule type: mRNA
A:Residues: 1-1306 <SOU>
A:Cross-references: GB:J04144; NID:g178285; PIDN:AAA51684.1; PID:g178286
A:Experimental source: kidney
A:Note: parts of this sequence, including the amino end of the mature protein, were derived from a cDNA clone of the human angiotensin I-converting enzyme, H. Takeuchi, K.; Shimizu, T.; Ohishi, N.; Seyama, Y.; Takaku, F.; Yotsumoto, H. J. Biochem. 106, 442-445, 1989
A:Title: Purification of human lung angiotensin-converting enzyme by high-performance liquid chromatography
A:Reference number: PQ0004; MUID:90110025; PMID:2558109
A:Accession: PQ0004
A:Molecule type: protein
A:Residues: 'XX', 32-34, 'E', 36-37, 'X', 39-41, 'R', 43-46 <TAK>
A:Experimental source: lung
C:Comment: This splice form is found in many tissues, in particular kidney and lung
C:Genetics:
A:Gene: GDB:DCPI; ACE
A:Cross-references: GDB:119840; OMIM:106180

A:Accession: A29220
A:Molecule type: mRNA
A:Residues: 1-332 <BE2>
A:Cross-references: GB:J03940; NID:G191593; PIDN:AAA7146.1; PID:G191594
R:Bernstein, K.E.; Martin, B.M.; Striker, L.; Striker, G.
Kidney Int. 33, 652-655, 1988
A:Title: Partial protein sequence of mouse and bovine kidney angiotensin converting enzyme
A:Reference number: A61477; MUID:88215372; PMID:2835538
A:Accession: A61477
A>Status: preliminary
A:Molecule type: protein
A:Residues: 35-54 <BE3>
A:Experimental source: kidney
C:Superfamily: mammalian peptidyl-dipeptidase A
C:Keywords: alternative splicing; blood pressure control; membrane protein; peptidyl-dipeptidase A
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-1312/Product: peptidyl dipeptidase I #status predicted <MAT>

Query Match 31.1%; Score 1334; DB 1; Length 1312;
Best Local Similarity 42.6%; Pred. No. 9.3e-84;
Matches 255; Conservative 112; Mismatches 213; Indels 18; Gaps 7;

QY 20 TIEQAKFLDFENHEADLFYQSSLASWNTNTITEENVQNNAGDKWAFLEQSTL 79
DB 649 TDEAKDRFVEYDRTAQVLLNEYAEANQYNTIIEGSKILLEKSTEVSHILKYGR 708

QY 80 AQMYPLQEIQNTLVKQLQALQOQSSVLSSEKSKRLNTILNTMTSTYSGKVCNPNPQ 139
DB 709 AKTFDVSQNSIKRIKKQLNDRAVLPPKELESEYNQILDMETTYSLNICYNG-- 766

QY 140 ECILLEPGLNEIMANSLDYNRLWAWESRVSQKQLRPLVEEYVVLKNEVARANHYEDY 199
DB 767 TCMLEPDLTNNMATSRYEELLWAKSRDVGRAILPFPKYVPEPSKIAKNGYIDA 826

QY 200 GDYWRGDYEVNGVDGYDSRGQLIEDVEHTFEEIKPLHYHLHAYVRKLMNAYPS-YISP 258
DB 827 GDSWRSLYESDNLE-----QDLEKLYQELQPLYLNLHAYVRRSLRHRYGSEYINL 876

QY 259 IGLPFAHLGDMWGRFWTNLYSLITVPFGQKPNIDVTDMVDQAWDAQRIKFAEKFFVS 318
DB 877 DGIPIAHLGDMWGRFWTNLYSLITVPFGQKPNIDVTDMVDQAWDAQRIKFAEKFFVS 936

QY 319 GLPNMTQGFWNSMLTDPGNQKAVCHPTAWDLGKG-DPRILMCTKVMTDDPLTAHHEMG 377
DB 937 GLLPVPEFNNKSMLEKPTDGRVWCHPSAWDFYNGKDFRIKQCTSVNMEDIVIAHHEMG 996

QY 378 HIQYDMAYAAQPLLRNGANEGFHAEGEIMSLSAATPKHLKSIIGLLSPDFQEDNTEI 437
DB 997 HIQYFMQYKDLPTVFREGANEGFHAEGEIMSLSAATPKHLKSIIGLLSPDFQEDNTEI 1055

QY 438 FLKQALTIIVGTLPFTYMLEKRWVFKGEIPKQDMKKWEMKREIVGVVPEVPHDET 497
DB 1056 FLKQALTIIVGTLPFTYMLEKRWVFKGEIPKQDMKKWEMKREIVGVVPEVPHDET 1115

QY 498 CDPAFLHVSNDYSFIRYTRTYQFQFQALCOAAKHEGPHLKCDISNSTEAGOKLFN 557
DB 1116 FDPGSKFHPANVPYIRYFVSVFIQFQFQALCOAAKHEGPHLKCDISNSTEAGOKLFN 1175

QY 558 LRLKSEPTWTLALENVVQAKNNVRPLLNYFEPLTWLKDQNK--NSFVGW-STDWSP 612
DB 1176 MCLGSKPWPPEAMKLIITGQPNMSASAMNRYFKPLTEWLVTENRRHGETLGPWPNWAP 1233

RESULT 6
JC2489
peptidyl-dipeptidase A (BC 3.4.15.1) - chicken
N:Alternate names: angiotensin converting enzyme
C:Species: Gallus gallus (chicken)
C:Date: 16-Mar-1995 #sequence_revision 26-May-1995 #text_change 28-May-1999
C:Accession: JC2489
R:Bernstein, K.E.; Thomas Jr., K.E.; Bernstein, K.E.
Biochem. Biophys. Res. Commun. 205, 1916-1921, 1994
A:Title: Chicken lacks the testis specific isozyme of angiotensin converting enzyme found

A:Reference number: JC2489; MUID:95110342; PMID:7811282

A:Accession: JC2489

A:Molecule type: mRNA

A:Residues: 1-1193 <EST>

A:Cross-references: GB:L40175; NID:G685169; PIDN:AAA75554.1; PID:G994708

C:Comment: This enzyme is a zinc dependant dipeptidyl carboxypeptidase that cleaves a

C:Superfamily: mammalian peptidyl-dipeptidase A

C:Keywords: metal binding; peptidyl-dipeptide hydrolase; zinc

F:316,331,914,929/Binding site: zinc, catalytic (Glu, His, Glu, His) #status predicted

Query Match 30.6%; Score 1312; DB 2; Length 1193;

Best Local Similarity 40.4%; Pred. No. 2.7e-82;

Matches 264; Conservative 110; Mismatches 243; Indels 36; Gaps 10;

QY 22 EQAKTFLDKFHEADLFYQSSLASWNTNTITEENVQNNAGDKWAFLEQSTLAQ 81

DB 544 EAQAEFLSEYNSTAEVNNAYTEASWEYNTNITDHNKEVMDLEKMLAKSKHTIEVGMAR 503

QY 82 MYPLQEIQNTLVKQLQALQOQSSVLSSEKSKRLNTILNTMTSTYSGKVCNPN--P 138

DB 604 QDPSPDFQETVTRILNKLVLERAALPEDELKYNLLSDMETTYSVAKVCRENTHP 663

QY 139 QECILLEPGLNEIMANSLDYNRLWAWESRVSQKQLRPLVEEYVVLKNEVARANHYED 198

DB 664 -----LDPDLTDLATSRDYNELLFAWKGMWDASGAKTKDKRYVVELSKAAVLNGYTD 718

QY 199 YGDYWRGDYEVNGVDGYDSRGQLIEDVEHTFEEIKPLHYHLHAYVRKLMNAY-PSYS 257

DB 719 NGAYWSLSETPTFE-----EDLERLYQLQPLYLNLHAYVRRALYNYKYGAEHTS 768

QY 258 PIGCLPAHLGDMWGRFWTNLYSLITVPFGQKPNIDVTDMVDQAWDAQRIKFAEKFFVS 317

DB 769 LKGPFAHLGDMWGRFWTNLYSLITVPFGQKPNIDVTDMVDQAWDAQRIKFAEKFFVS 828

QY 318 VGLPNMTQGFWNSMLTDPGNQKAVCHPTAWDL-GKGDPRILMCTKVMTDDPLTAHHEM 376

DB 829 LGLIPMPQEFWDKSMTEKADGREVVCHASAWDFYNRKDFRIKQCTVVMNDDLIIVHEM 888

QY 377 GHQYDMAYAAQPLLRNGANEGFHAEGEIMSLSAATPKHLKSIIGLLSPDFQEDNTEI 436

DB 889 GHVQYFLQYMDQPISTPRDGANPGFHEAIGDMWALSVPKHLHSINLLD-QVTENEESDI 947

QY 437 NFLLKQALTIIVGTLPFTYMLEKRWVFKGEIPKQDMKKWEMKREIVGVVPEVPHDET 496

DB 948 NYLMSIALDKIAFLPFGYLMQWRKVFQDRIEDEVNQWNNLRLKYQGLCPFPVRSERD 1007

QY 497 YCDPASLHVSNDYSFIRYTRTYQFQFQALCOAAKHEGPHLKCDISNSTEAGOKLFN 556

DB 1008 DFDPGAKFHPANVPYIRYFVSVFIQFQFQALCOAAKHEGPHLKCDISNSTEAGOKLFN 1067

QY 557 MLRLKSEPTWTLALENVVQAKNNVRPLLNYFEPLTWL--KDQNKNSFVGW-STDWSPY 613

DB 1068 AMKLGSKPWPPEAMKLIITGQPNMSAEALMSYFPEPLMTWLKKNTENGCEVLGWEYSWTPY 1127

QY 614 ADQSIKVRISLSKALG-----DKAYEWNENKYLFRSSVAVAMROYFLKVK 659

DB 1128 AVTEFHAATDADFLGMSVGTQKATAGAW-----VLLALALAVLITSIPLGVK 1175

RESULT 7

JC2038

peptidyl-dipeptidase A (BC 3.4.15.1) - rat

N:Alternate names: angiotensin converting enzyme; kinase II

C:Species: Rattus norvegicus (Norway rat)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: JC2038

R:Koike, G.; Krieger, J.E.; Jacob, H.J.; Mukoyama, M.; Pratt, R.E.; Dzau, V.J.

Biochem. Biophys. Res. Commun. 198, 380-386, 1994

A:Title: Angiotensin converting enzyme and genetic hypertension: Cloning of rat cDNAs

A:Reference number: JC2038; MUID:94121658; PMID:8292044

C:Accession: JC2038

A:Molecule type: mRNA

A:Residues: 1-1313 <KOI>

A;Cross-references: GB:U03734; NID:9437289; PIDN:AAA82111.1; PID:9437290
 A;Note: the authors translated the codon ACC for residue 159 as Tyr
 C;Comment: This enzyme is a zinc-containing dicarboxy peptidase that cleaves angiotensin I
 C;Comment: This enzyme plays a critical role in blood pressure homeostasis and is the ta
 C;Superfamily: mammalian peptidyl-di-peptidase A
 C;Keywords: alternative splicing; peptidyl-di-peptide hydrolase; transmembrane protein; z
 F;993-400,990-998/Region: catalytic #status predicted
 F;1264-1284/Domain: transmembrane #status predicted <TM>

Query Match 30.5%; Score 1310; DB 1; Length 1313;
 Best Local Similarity 42.0%; Pred. No. 4.2e-82;
 Matches 251; Conservative 115; Mismatches 214; Indels 18; Gaps 7;

QY 20 TIEQAKTFLDPKFNHEADLFYQSSLASWNTNITTEVQNMNAGDKSAFLKEOSTL 79
 DB 650 TDEAKNRVEYDYRTAKVLMWEAEANWNTNITTEGSKILLQKKEVSNHTLKYGTV 709
 QY 80 AQMYPLQEIQNTLVKLOLQALQNGSSVLSEDSKRLNTILNTMTSTIYSTGKVCNPNQ 139
 DB 710 AKTFDVSNFQNSTIKRIIKVQNVDRVLPNNELEYNQILLDMETIYSVANVCYNG-- 767
 QY 140 ECLLPGLNEIMANSLDYNERLWAWSEVQKQLRPLVEEYVVLKNEMARANHYEDY 199
 DB 768 TCLSEPDLTNIMATSRKYEEALLWKSWRDKVGRAILPFPFKYVDFSNKIANGYSDA 827
 QY 200 GDYWRGDYEVNGVDGYDSRGQIEDVEHTPEEIKPLYLHAYVRAKLNAVPS-YISP 258
 DB 828 GDSWRSSYESDLE-----QDLKLYQELQPLYNLHAYVRSLSHRHYSEYINL 877
 QY 259 ICLPAHLIGDMWGRFWNTLYSLTVFGQKNIDVTDMVDQANDQADRIKAEKFFVS 318
 DB 878 DGPIPAHLGNNMAQTSNIDVLAFFPSAPSIDATEAMIKQGTWPRIRKEADNFTSL 937
 QY 319 GLPNNTQGFWNSMLTDPGNVQKAVCHPTAMDLGK-DFRILMCTKVTMDDFLTAHEMG 377
 DB 938 GLLPVPPEFWNKSMLKPTDGRVNVCHASAWDFYNGKDFRIKQCTSVNMEELVIAHEMG 997
 QY 378 HLYQDMAYAAQPFLLRNGANGFHEAVGEIMSLNAPFKHLSIGLLSPFQEDNEFEIN 437
 DB 998 HLYQFMQYKDLPTVTFREGANPGFHEAGDVIALSVSTPKHLHSINLSS- GSGYEHDIN 1056
 QY 438 FLKQALITVGLPTTYMLEKRWNVFKGEIPKQMKMKWEMREKREIVGVVPEVPHDET 497
 DB 1057 FLMKWALDKIAIFPFSYLLIDWNRVDFGSIKENYQNWESLRLKYQGLCPVPRSQGD 1116
 QY 498 CPASLHVSNDYSPIRYVTRTYLQFOFQEQALCOAAKHGDLHKCDISNSTEAGQKLFNM 557
 DB 1117 FPGSKFHPANVPVIRVFISFIIOFQHEALCAAAGHTGLPKYCDIYQSKBAGKLADA 1176
 QY 558 LRLGKSEPTLALENVGAKNNVRPLNLYFEPLFTWLKQNK--NSFVGW-STDWSP 612
 DB 1177 MKLGYSKQWPEAKKIITQPNMSAGAIMNYFKPLTEMLVTENRRHGETLGMPEYTWTF 1234

RESULT 8
 A34402
 N;Alternate names: angiotensin I-converting enzyme; dipeptidyl carboxypeptidase I; pepti
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: A34402; A60724; A36232; C18700
 R;Kumar, R.S.; Kusari, J.; Roy, S.N.; Soffer, R.L.; Sen, G.C.
 J. Biol. Chem. 264, 16754-16758, 1989
 A;Title: Structure of testicular angiotensin-converting enzyme. A segmental mosaic isozy
 A;Reference number: A34402; MUID:89380303; PMID:2550457
 A;Accession: A34402
 A;Molecule type: mRNA
 A;Residues: 1-737 <XM>
 A;Cross-references: GB:J05041; NID:9164744; PIDN:AAA31153.1; PID:9164745
 R;Sen, G.C.; Thakkumkara, T.J.; Kumar, R.S.
 J. Cardiovasc. Pharmacol. 16(Suppl.4), S14-S18, 1990
 A;Title: Angiotensin-converting enzyme: structural relationship of the testicular and the
 A;Reference number: A60724; MUID:91155372; PMID:1705622

A;Accession: A60724
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 73-173 <SN>
 A;Note: identical sequences were obtained for mRNAs from lung and testes
 R;Chen, Y.N.P.; Riordan, J.F.
 Biochemistry 29, 10493-10498, 1990
 A;Title: Identification of essential tyrosine and lysine residues in angiotensin conver
 A;Reference number: A36232; MUID:91104959; PMID:2176870
 A;Accession: A36232
 A;Molecule type: protein
 A;Residues: 154-160;236-242 <CH>
 R;Iwata, K.; Lai, C.Y.; El-Dorri, H.A.; Soffer, R.L.
 Biochem. Biophys. Res. Commun. 107, 1097-1103, 1982
 A;Title: The NH2- and COOH-terminal sequences of the angiotensin-converting enzyme isozy
 A;Reference number: A90107; MUID:83048249; PMID:6291514
 A;Accession: C18700
 A;Molecule type: protein
 A;Residues: 33-35; 'SN'; '38-39; 'SS'; 'FAEL'; '737 <IWA>
 A;Note: several of the amino acids in reported are tentative
 C;Comment: The pulmonary and testicular isoforms of this enzyme differ substantially in
 ggests that the two isoforms arise by alternative splicing of one gene.
 C;Superfamily: mammalian peptidyl-di-peptidase A
 C;Keywords: alternative splicing; peptidyl-di-peptide hydrolase; testis; transmembrane pr

Query Match 29.9%; Score 1283; DB 1; Length 737;
 Best Local Similarity 40.8%; Pred. No. 1.3e-80;
 Matches 250; Conservative 112; Mismatches 213; Indels 38; Gaps 10;

QY 20 TIEQAKTFLDPKFNHEADLFYQSSLASWNTNITTE-----NVQNMN--AGDKW 69
 DB 75 TDEAKSRFVEYDPSQAVNWEAEANWNTNITTEASKILLQKNNQIANHTLYGNW 134
 QY 70 SAFLKEOSTLAQMYPLQEIQNTLVKLOLQALQNGSSVLSEDSKRLNTILNTMTSTIYST 129
 DB 135 -----ARRFDVSNFQNSTIKRIIKVQDLQRAVLPVKEEYNQILLDMETIYSV 184
 QY 130 GKVCNPNQPCILLEGELNEIMANSLDYNERLWAWSEVQKQLRPLVEEYVVLKNE 199
 DB 185 ANVCRRVDG--SCLEQEPDLTNLMATSRKYDELLWMTSWRDKVGRAILPFPFKYVEFTNK 242
 QY 190 MARANHYEDYGDYWRGDYEVNGVDGYDSRGQIEDVEHTPEEIKPLYLHAYVRAKLM 249
 DB 243 AARLNGYVDAGDSNRSMYETPTLE-----QDLERLFQELQPLYNLHAYVGRALH 292
 QY 250 NAY-PSYISPTGCLPAHLIGDMWGRFWNTLYSLTVFGQKNIDVTDMVDQANDQADRIE 308
 DB 293 RHYGAQHINLEGP:PAHLGNNMAQTSNIDVLAFFPSAPSIDATEAMIKQGTWPRIRMF 352
 QY 309 KEAEKFFVSGLPNNTQGFWNSMLTDPGNVQKAVCHPTAMDLGK-DFRILMCTKVTMD 367
 DB 353 EADKFFISLGLLPVPPEFWNKSMLKPTDGRVNVCHASAWDFYNGKDFRIKQCTTVNME 412
 QY 368 DFLTAHEMGHIQYDMAYAAQPFLLRNGANGFHEAVGEIMSLNAPFKHLSIGLLSPD 427
 DB 413 DLVVVHHMGHIQYFMQYKDLPTVTFREGANPGFHEAGDVIALSVSTPKHLHSINLSS 472
 QY 428 FQEDNEFEINFLKQALITVGLPTTYMLEKRWNVFKGEIPKQMKMKWEMREKREIVGV 487
 DB 473 -GGGYEHDINFLMKWALDKIAIFPFSYLVDEWNRVDFGSIKENYQNWESLRLKYQGL 531
 QY 488 VERYPHDETCDPASLHVSNDYSPIRYVTRTYLQFOFQEQALCOAAKHGDLHKCDISN 547
 DB 532 CPPAPRSQGDPPGAKFHIPSSVPIRYVFISFIIOFQHEALCAAAGHTGLPKYCDIYQS 591
 QY 548 TEAGQKLFNMLRLGKSEPTLALENVGAKNNVRPLNLYFEPLFTWLKQNK--KNSFVG 605
 DB 592 KEAGKRLADAMKLGYSKFWPEAKMVKITQPNMSASAMNYFKELMDWLLTENGHRGHEKLG 651
 QY 606 W-STDWSPYADQS 617
 DB 652 WPQYTWTPNSARS 664

RESULT 9
S35484
peptidyl-dipeptidase A (EC 3.4.15.1) precursor, pulmonary splice form - rabbit
N;Alternate names: angiotensin-converting enzyme; dipeptidyl carboxypeptidase I; kininase
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S35484; A23455; A18700; A38655; A49726; S17509
R;Thakumkara, T.J.; Livingston III, W.; Kumar, R.S.; Sen, G.C.
Nucleic Acids Res. 20, 683-687, 1992
A;Title: Use of alternative polyadenylation sites for tissue-specific transcription of the
A;Reference number: S35484; MUID: 92178960; PMID:1311831
A;Accession: S35484
A;Molecule type: mRNA
A;Residues: 1-1309 <THE>
A;Cross-references: EMBL:X62551
R;Iwata, K.; Blacher, R.; Soffer, R.L.; Lai, C.Y.
Arch. Biochem. Biophys. 227, 188-201, 1983
A;Reference number: A23455; MUID: 84051289; PMID:6314908
A;Accession: A23455
A;Molecule type: protein
A;Residues: 34-47, N, 49-55 <IWA>
A;Experimental source: lung
R;Iwata, K.; Lai, C.Y.; El-Dorriy, H.A.; Soffer, R.L.
Biochem. Biophys. Res. Commun. 107, 1097-1103, 1982
A;Title: The NH2- and COOH-terminal sequences of the angiotensin-converting enzyme isozym
A;Reference number: A90107; MUID: 83048249; PMID:6291514
A;Accession: A18700
A;Molecule type: protein
A;Residues: 34-44, 754-755, L, 757 <IWI>
R;Kumara, R.S.; Thakumkara, T.J.; Sen, G.C.
J. Biol. Chem. 266, 3854-3862, 1991
A;Title: The mRNAs encoding the two angiotensin-converting isozymes are transcribed from
A;Reference number: A38655; MUID: 91139683; PMID:1847388
A;Accession: A38655
A;Molecule type: DNA
A;Residues: 1-88 <KUM>
A;Cross-references: GB:M58579
R;Ranchandran, R.; Sen, G.C.; Misano, K.; Sen, I.
J. Biol. Chem. 269, 2125-2130, 1994
A;Title: Regulated cleavage-secretion of the membrane-bound angiotensin-converting enzym
A;Reference number: A49726; MUID: 94124568; PMID:8294466
A;Accession: A49726
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1236-1258 <RAM>
A;Experimental source: testis
R;Kirley, T.L.
Biochem. J. 278, 375-380, 1991
A;Title: The Mg(2+)-ATPase of rabbit skeletal-muscle transverse tubule is a highly glyco
A;Reference number: S17509; MUID: 91378880; PMID:1654880
A;Accession: S17509
A;Status: preliminary
A;Molecule type: protein
A;Residues: 34-55 <KIR>
C;Comment: This enzyme converts angiotensin I to angiotensin II in presence of divalent
ver, the enzyme has been found also in renal tubules and intestinal mucosa.
C;Superfamily: mammalian peptidyl-dipeptidase A
C;Keywords: alternative splicing; blood pressure control; chloride; glycoprotein; intest
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-1309/Product: peptidyl-dipeptidase A, pulmonary #status experimental <MAT>
F;59,79,150,322,448,512,680,717,945,1194/Binding site: carbohydrate (Asn) (covalent)

Query Match 29.8%; Score 1283; DB 1; Length 1309;
Best Local Similarity 40.8%; Pred. No. 3.1e-80;
Matches 250; Conservative 112; Mismatches 213; Indels 38; Gaps 10;
QY 20 TIEEAKTFLDKFNHEADLFYQSSLASWNTNITEE-----NVQNMN--AGDKW 69
DB 647 TDEAASRFEYEDRSFQAVNWEAEANWNTNITEASKILLQKNQIANHTLYGNW 706
QY 70 SAPLKEOSTLAQMYPLQEQINLVKVLQALQNGSSVLSDEKSKRLNTILNTWSTIYST 129

707 -----ARRFDVSNFQNAKSKRIKKYQDLQRAVLPMKELEYNQILLDMETIYSV 756
QY 130 GAVCPNDPQECCLLEPCNEIMANSIDYNERIWAWESEVSGKQLRPLVEEYVLKNE 189
DB 757 ANVCRVDG--SCLEPDLTWMATSKYDELLVWTSWRDKVGRALPFPFKVETNK 814
QY 190 MARANHYEDGYMGDVEYNGVGDYSGRQLLEDVEHTFEETKPLYEHLHAYVRKLM 249
DB 815 AARLNGYVDAGDSWRMYETETLE-----QDLERLFQELQPLYLNLHAYVGRALH 864
QY 250 NAY-PSYISPIGCLPAHLGLDGMWGRFNTNLSYLVFPGQKPNIDVTDMYDQAWDAORIF 308
DB 865 RHYGQHINLEGPIDAHLLGNWAGTWSNIYDLVAPPSASTMDATEAMIKQGTTPREMF 924
QY 309 KEAEKFFVSGVGLPNTQGFWNSMLTDPGNVQKAVCHPTAWDLGKG--DFRILMCTKTMD 367
DB 925 EEADEKFFISLGLLPVPPEFNNKSMLEKPTDGRVYVCHASAWDFYNGKDFRIKQCTTVMNE 984
QY 368 DELTAHEHMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPFKILKSLGLLSPD 427
DB 985 DLVVVHEHMGHIQYFMQYKDLFVALREGANPGFHEAIGDVLALSVSTPKHLHSINLLSSE 1044
QY 428 FOEDNETEINFLKQALITVGLTLPFTYMLEKRWNVFKGIPKQDQWKKWEMKREIVGV 487
DB 1045 -GGYSEHDINFLMKQWALDKIAFIPFSLVDEWRVRVFDGSITKENYNOEWSURLKYQGL 1103
QY 488 VEPVPHDETYCDPASLPHVSNIDYFIRYTRTLTYQFQEQALCOAAKEGPHLKHCDISNS 547
DB 1104 CPPAPRSQGDFFGAKFHPSSVPIRVFVSFIQFQHEALCKAAGTGPLHTCDIYQS 1163
QY 548 TEAGQKLFNMLRLGSEFWTLALENVGAKMNVRLPILNYPEPLFTWLKQDN--KNSFVG 605
DB 1164 KEAGKELADAMKLGYSKWPPEAMKVTITQPNMSASAMWYFKPLMDMLLTENGHRHGEKIG 1223
QY 606 W-STDWSPYADQS 617
DB 1224 WPQYTWTPNSARS 1236

RESULT 10
S65472
peptidyl-dipeptidase A (EC 3.4.15.1) precursor - horn fly
N;Alternate names: angiotensin I-converting enzyme
C;Species: Haematobia irritans (horn fly)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 22-Jun-1999
R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen,
Eur. J. Biochem. 237, 414-423, 1996
A;Title: Cloning and characterisation of angiotensin-converting enzyme from the dipter.
A;Reference number: S65431; MUID: 96215437; PMID:8647080
A;Accession: S65472
A;Molecule type: DNA
A;Residues: 1-611 <WIJ>
A;Cross-references: EMBL:L43965; NID:G908759; PIDN:AAA70427.1; PID:G908760
A;Note: the source is designated as Haematobia irritans exigua
A;Accession: S65431
A;Molecule type: protein
A;Residues: 18, P, 20-42; 75-77, Q, 79-81, X, 83-84; 179-190 <WIW>
A;Note: the source is designated as Haematobia irritans exigua
C;Genetics:
C;Gene: ACE
C;Superfamily: mammalian peptidyl-dipeptidase A
C;Keywords: glycoprotein; metal binding; peptidyl-dipeptide hydrolase; zinc
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-611/Product: peptidyl-dipeptidase A #status predicted <MAT>
F;53,196,531/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 24.7%; Score 1058; DB 2; Length 611;
Best Local Similarity 37.2%; Pred. No. 3.5e-65;
Matches 223; Conservative 108; Mismatches 246; Indels 22; Gaps 7;
QY 8 LLSLVAVTAQSTIEEQAFLDKFNHEADLFYQSSLASWNTNITEE NVQNMNAGD 67

Db 8 ILAGLVCHGATKEEIVATEYLQINIKELAKHTNVTETVSWAYSNITDENRLENSA 67
 Qy 68 KNSAFLEKEOSTLAQMPLOEIQNLTVKLOLQALQONGSVLSSEKSKRLNTILNTMTIY 127
 Db 68 ENAKFLKEVAKOIQKFNWYTGSDVRRQFKSLSTGYSAIPAEDYAEELLEVLGAMESNF 127
 Qy 128 STGKVCNPNPOBC-LLLPGLNEIMANSLDYNERLMAWESWRSEVKGQKQLRPLYEEYVVL 186
 Db 128 AKRVCDYKNSAKCDLSLOPEIEEIIITKSRDPEELKYWTQFYDKAGTPTSRNFEKYVEL 187
 Qy 187 KNEMARANHVEDYDGYWRGDEYVNGVDYDSRGQLIED-VEHTFEETKPLYEHLHAYR 245
 Db 188 NTSKALNNFTDGAENVLDEYE-----DATFEDQLEAIPEDIKPLYDQVHGVR 236
 Qy 246 AKLMNAY-PSYISPIGCLPAHLGDMWGRFNTNLSLTVPGQKFNIDVTDMYDQAWDA 304
 Db 237 YRLNKFYGVDEWVSKTGPLPMHLLGNWAOQWSSIAIVSPPEKPLVDVSDVMAQGYTP 296
 Qy 305 QRIFKEAEKFFVSVGLPNNTOGFENSMILTDPGNVQKAVCHPTAWDLG-KGDFILACTK 363
 Db 297 LKWFQMGDDFFQSMGLKKLPQEFWDKSLDEKDDGDLVCHASAWDFYLTDDVRIKQCTR 356
 Qy 364 VTMDDELTAHEHGHIOYDMAYAAQFLLRNGANEGPHEAAGEIMSLSAATPKHLKISGL 423
 Db 357 VTQDQFVTHHEHGHIOYFLOVQHPFVYRTGANPGFHEAVGDVLSLSVSTPKELRVGL 416
 Qy 424 LSPDFQEDNETEINFLLKQALITVGLPFTYMLEKRWVMPKGEIPKQDMWKKWEMKREI 483
 Db 417 LK-NYVSDNEARINQLFTALDKIVLPFAFTMDKRYMSLFRGEYDKANMNCATFWKLREY 475
 Qy 484 IGVVPEVPFHDEYCDPASLFHVSNDYSFIRYRTLYQFOFQOALCOAA-----RHEG 537
 Db 476 YSGIEPPVVRTEKDFDAPAKYHVSADVEYLRVLSFIIQFOFYKSACITAGETVYVNTQY 535
 Qy 538 PLHKCDISNSTEAGOKLFNMLRGLKSEFWTLAENVGAKMNVRLNLYPEPLFTWIK 596
 Db 536 PLONCDIYGSKEAGKLFENMLSLGASKPMPDALEAFNGERIMSGKATAEYFEPLRVMLE 594

RESULT 11

peptidyl-dipeptidase A (EC 3.4.15.1) 67k precursor - fruit fly (Drosophila melanogaster),
 N;Alternate names: angiotensin-converting enzyme
 C;Species: Drosophila melanogaster
 C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 26-Feb-1998
 C;Accession: A57533
 R;Cornell, M.J.; Williams, T.A.; Lamango, N.S.; Coates, D.; Corvol, P.; Soubrier, F.; R
 J. Biol. Chem. 270, 13613-13619, 1995
 A;Title: Cloning and expression of an evolutionary conserved single-domain angiotensin d
 A;Reference number: A57533; MUID:95293950; PMID:7775412
 A;Accession: A57533
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-615 <COR>
 A;Cross-references: GB:U25344
 C;Genetics:
 A;Gene: FlyBase:Ance
 A;Cross-references: FlyBase:Fgn0012037
 C;Superfamily: mammalian peptidyl-dipeptidase A
 C;Keywords: peptidyl-dipeptide hydrolase

Query Match 24.2%; Score 1039; DB 2; Length 615;
 Best Local Similarity 35.8%; Pred. No. 7.3e-64;
 Matches 219; Conservative 120; Mismatches 251; Indels 22; Gaps 9;

Qy 8 LLSLVAVTAQSTIEBOAKTFELDKFNHEAEDLFYQSSLASWNTNTNTEENVQNNAGD 67
 Db 8 LLATLAVTQALVKEIQAEYLENLKELAKRTNVTETEAAYGNSITDENKKEISEA 67
 Qy 68 KNSAFLEKEOSTLAQMPLOEIQNLTVKLOLQALQONGSVLSSEKSKRLNTILNTMTIY 127
 Db 68 ELAKFMKEVASDTTKQFWYSQSEDLKQFQKALTKLGAALFEDDYLAEELLDTLGAESNF 127

Qy 128 STGKVCNPNPOBC-LLLPGLNEIMANSLDYNERLMAWESWRSEVKGQKQLRPLYEEYVVL 186
 Db 128 AKRVCDYKNSAKCDLSLOPEIEEIIITKSRDPEELKYWTQFYDKAGTPTSRNFEKYVEL 187
 Qy 187 KNEMARANHVEDYDGYWRGDEYVNGVDYDSRGQLIED-VEHTFEETKPLYEHLHAYR 246
 Db 188 NTSKALNNFTDGAENVLDEYE-----DATFEDQLEAIPEDIKPLYDQVHGVR 237
 Qy 246 AKLMNAY-PSYISPIGCLPAHLGDMWGRFNTNLSLTVPGQKFNIDVTDMYDQAWDA 305
 Db 237 YRLNKFYGVDEWVSKTGPLPMHLLGNWAOQWSSIAIVSPPEKPLVDVSDVMAQGYTP 297
 Qy 305 QRIFKEAEKFFVSVGLPNNTOGFENSMILTDPGNVQKAVCHPTAWDLG-KGDFILACTK 364
 Db 297 LKWFQMGDDFFQSMGLKKLPQEFWDKSLDEKDDGDLVCHASAWDFYLTDDVRIKQCTR 357
 Qy 364 VTMDDELTAHEHGHIOYDMAYAAQFLLRNGANEGPHEAAGEIMSLSAATPKHLKISGL 424
 Db 357 VTQDQFVTHHEHGHIOYFLOVQHPFVYRTGANPGFHEAVGDVLSLSVSTPKELRVGL 417
 Qy 424 LSPDFQEDNETEINFLLKQALITVGLPFTYMLEKRWVMPKGEIPKQDMWKKWEMKREI 484
 Db 417 LK-NYVSDNEARINQLFTALDKIVLPFAFTMDKRYMSLFRGEYDKANMNCATFWKLREY 476
 Qy 484 IGVVPEVPFHDEYCDPASLFHVSNDYSFIRYRTLYQFOFQOALCOAA-----RHEG 538
 Db 476 YSGIEPPVVRTEKDFDAPAKYHVSADVEYLRVLSFIIQFOFYKSACITAGETVYVNTQY 536
 Qy 538 PLHKCDISNSTEAGOKLFNMLRGLKSEFWTLAENVGAKMNVRLNLYPEPLFTWIK 598
 Db 536 PLONCDIYGSKEAGKLFENMLSLGASKPMPDALEAFNGERIMSGKATAEYFEPLRVMLE 596
 Qy 599 N-KNSFVGWST 608
 Db 597 NTKNNVHIGWIT 608

RESULT 12

JC5374
 angiotensin-converting enzyme-related protein - fruit fly (Drosophila melanogaster)
 C;Species: Drosophila melanogaster
 C;Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jul-2000
 C;Accession: JC5374
 R;Taylor, C.A.M.; Coates, D.; Shirras, A.D.
 Gene 181, 191-197, 1996
 A;Title: The Acer gene of Drosophila codes for an angiotensin-converting enzyme homolog
 A;Reference number: JC5374; MUID:97128790; PMID:8973330
 A;Accession: JC5374
 A;Molecule type: mRNA
 A;Residues: 1-630 <TAY>
 A;Cross-references: EMBL:X96913; NID:gl405881; PIDN:CAA65632.1; PID:gl405882
 C;Genetics:
 A;Gene: Acer
 C;Superfamily: mammalian peptidyl-dipeptidase A

Query Match 24.0%; Score 1030; DB 2; Length 630;
 Best Local Similarity 35.6%; Pred. No. 3.2e-63;
 Matches 219; Conservative 113; Mismatches 260; Indels 24; Gaps 10;

Qy 6 WLLSLVAVTAQSTIEBOAKTFELDKFNHEAEDLFYQSSLASWNTNTNTEENVQNNNA 65
 Db 16 WLPGLSGNCSASVLE-ARRFELENEQLRRRFFHEEFLSGYNYNTNTNTEANQAMIEV 74
 Qy 66 GDKWSAFLEKEOSTLAQMPLOEIQNLTVKLOLQALQONGSVLSSEKSKRLNTILNTMT 125
 Db 75 YARNAELNKLAAQTKSSDYVQSEDAIRRQAEHLKLGASALNADDYALQALOAISMQT 134
 Qy 126 IYSTGKVCNPNPOBC-LLLPGLNEIMANSLDYNERLMAWESWRSEVKGQKQLRPLYEEYV 184
 Db 135 NYATATVCSYTNRSDCSLTLEPHIQERLSHRDPAELAWYREWHDKSGTFPMQNFAYV 134
 Qy 185 VLKNEARANHVEDYDGYWRGDEYVNGVDYDSRGQLIEDVEHTFEETKPLYEHLHAYV 244

Db 195 RLTRKASQLNGHRSYADYVWQFYB-----DPPDER-----QLDATEKQLPLPLYRLHGVV 244
 QY 245 RAKLMNAY-PSYISPIGCLPAHLIGDMGGRFVWNLVSLTVPPGQKKNIDVTAMVDQAWD 303
 Db 245 RFRIRQHYGPDVMPAEGNIPISLGNMWSWNLDELFTPYPEKPFVDVKAEMKQGYT 304
 QY 304 AQRIFKBAEKFFSVGLPNNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGK-GDFRILMCT 362
 Db 305 VOKLFELGDQFQSLGRALPPSPWNLVSLTRPDD-RQVVCHASANDFYQDSVDVRIKMT 363
 QY 363 KVTWDDFLTAHENGCHTOYDAYAAQFLLRNGANGFHEAVEIMSLSAATPKHLKSG 422
 Db 364 EVDGSHFYVHHELGHIQYLYQVEQQPAVYRGAPNPGFHEAVGDVIALSVMSAKHLKATG 423
 QY 423 LLSPDFQEDNTEINFLKQALITVGLPFTYMLEKRWMMVFRGEIPKQWMMKQWEMKR 482
 Db 424 LIE-NGLRDEKSRINQLFKQALSIVFLPGYAVDKYRVAVFNELDESQWNGFQWMS 482
 QY 483 EIVGVPEVPVPHDETCYPASLPHVSNDSYFIRYTRTLVQFQOEALCOAKHEGP-----538
 Db 483 EFGGVEPPVFTKDFDPPAKYHIDADVYLIRFAAHIFQFQHKVLCRRAGQYAPNNGR 542
 QY 539 --LHKCDISNSTEAGQKLFNMLRGKSEPTWLTALENVVGAKNMVRPLNYPFETWLK 596
 Db 543 LTLNCDIFGSKAAGRSLSQFLSKGNSRHWKEVLEBFTGETEMDPAALLEYPERLYOWLK 602
 QY 597 DQNKNSFVGVSTWSP 612
 Db 603 QE--NSRLGVPLGWP 616

RESULT 13

T15792
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
 C:Accession: T15792
 R:Hallsworth, K.
 submitted to the EMBL Data Library, April 1996
 A:Description: The sequence of C. elegans cosmid C42D8.
 A:Reference number: 218405
 A:Accession: T15792
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-907 <HAL>
 A:Cross-references: EMBL:U56966; NID:g1293844; PID:g1293847; PIDN:AAA98719.1; GSPDB:GN00
 A:Experimental source: strain Bristol N2; clone C42D8
 C:Genetics:
 A:Map position: X
 A:Introns: 140/3; 170/3; 194/3; 300/2; 467/3; 551/2; 600/2; 697/3; 774/2; 851/3

Query Match 15.0%; Score 642.5; DB 2; Length 907;
 Best Local Similarity 27.0%; Pred. No. 3.5e-36;
 Matches 172; Conservative 136; Mismatches 289; Indels 41; Gaps 19;
 QY 2 SSSSLLLSLVAVTAAGSTIEQAKTFLDRFNHEADLFYQSSLASWNYNTNITEENVQ 61
 Db 160 SSYWKTDNLQAPGSIKD--BEKLSWLAGYEAIAKVLREVALSGWRYFNDASPSLKA 217
 QY 62 MNAGDKWSAFLKEQSTLAQMYPLQEIQLTVKQLQALQONGSSVLSEDKSKRLNTILN 121
 Db 218 LDEAVLTMVFRSTMSQAKQFDMASVTDKVMKQLGYVFEFGSALAFSRFADYSQAOA 277
 QY 122 TWSTYISGKVCNPNPQECILLLEFGLNEINANSLDYNERLWAWESWRSEVGGKQLRPLYE 181
 Db 278 ALNRDSKDSSTICDKDVPPCALQIDMDSIFRNEKADSRQLHLVWSVYVTAIAKS-KFSYN 336
 QY 182 EYVVLKNSMARANYEDYGVWRGDYVNG-VDCGYDSRGLIEDVEHTFEETKPLYEHL 240
 Db 337 NIITISNGAKLNGFANGAMRSARFNDSSKVHKAEP---DLNKQIDKXISITQPIYQL 393
 QY 241 HAYVRAKLMNAY--PSYISPIGCLPAHLIGDMGGRFVWNLVSLTVPPGQKKNIDVTAMV 298

Db 394 HAYMRQLAGIYGNPVGLSKQGPPIFAHLFGSLDGDWNAHYEQTKPFEEES--ETPEAML 451
 QY 299 D-----QAWDAQRIKBAEKFFSVGLPNNMTQGFWNSMLTDPGNVQKAVCHP-TAWDL-G 352
 Db 452 SAFNTQNTYTKMFVYAYFYKFSAGPPLPKSYWTSIFARVWS-KDMICPAALADWRA 510
 QY 353 KGFPRILMCTKVTMDDFLTAHENGHIQYDMAAYAAQFLLRNGANGFHEAVEIMSLSA 412
 Db 511 PNDFRVKAQNLGEPDEQAHSLLVQYLYKQOSLLFREQASPVITDAIANAPAHLS 570
 QY 413 ATPKHLKSGILLSPDPQEDNTE-INFLKQALITVGLPFTYMLEKRWMMVFRGEIPKQ 471
 Db 571 TNPHTYLSQKLVPSHLIDKDSVIIKLYKESLEFTKLPTTIAADNRYLELDFDTVPKN 630
 QY 472 QWKKKWMEMKREIVGVVPEVPVPHDETCYPASLPH--VSNDSYFIRYTRTL-----YQPF 525
 Db 631 KLNDRWWEIRNKYEGVRSQPYPNTSLD--ALJHNSVSQVHS--PATRTLLISVYLKQI 685
 QY 526 QBALCOAA---KHGEPHLKCDISNSTEAGQKLFNMLRGKSEPTWLTALENVVGAKNMVR 582
 Db 686 LKALCORELFWLSEG-----CILSEDTT--EKLRMTKLGSSITWLKALEMISGKELDAQ 739
 QY 583 PLLNYPEPFLTMLKQNK--NSFVGVSTWSPYADQSI 618
 Db 740 PLLEYEPLINLWLNRTNEIDQVVGVGMDGSGTFTVEEI 777

RESULT 14

C83696
 hypothetical protein BH0371 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: C83696
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maui, N.; Fujii, F.; Hii
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: C83696
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-532 <STO>
 A:Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BA04090.1; GSPDB:GM
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH0371

Query Match 3.7%; Score 157; DB 2; Length 532;
 Best Local Similarity 21.1%; Pred. No. 0.0058;
 Matches 118; Conservative 83; Mismatches 213; Indels 144; Gaps 29;

QY 22 EQAKTFLDRFNHEADLFYQSSLASWNYNTNITEE-NVQNNMAGDKWSAFLKQS---77
 Db 3 EQDIERPLSQNRKVRDELQVPLLNHWVATTGGEWSDKHEQSLSEYWAHPSDRSQK 62
 QY 78 -----TLAQMYPLEIQNLTVKQLQALQONGSSVLSEDKSKRLNTILNTMTIY 127
 Db 63 VTRFRKIDSLLPMQRQLDLDDHKMKIKQFE--EGTQQOILSLE--KKISHVFTTFQPV 118
 QY 128 STGVKCNPNPQECILLLEPGLNEINANSLDYNERLWAWESWRSEVGGKQLRPLYEYVVLK 187
 Db 119 NGRVSNNE-----LLDILRYDLDRERKQAWFA-SKEVGKTEKDLQLIRK 166
 QY 188 NEWARANYEDYGVWRGDYVNGVGVYSGQLIEDVEHT---FEETKPIYEHHLHAYV 244
 Db 167 NEVARNLGPETF-----YHMSFATQELDEQFAMFETIKKSSDQAFRMI 211
 QY 245 -----RAKLMNAYPSYISPIGCLPAHLIGDMGGRFVWNLVSLTVPPGQK-PNIDVTDA 296
 Db 212 KDRIDERAKVZIKKDDLRP-----WDYVDPFPQEPAPSEHYD- 250
 QY 297 MVQAVDAQSIKFEAKKFFVSVGLPNNMTQGFWNSMLTDPGNVQK-AVCHPTAWDLGKGD 355

Db 251 -PDSFYKQDLQEVVSVQTFQAMLP---IDDLKSGSLYPRKNKNPFQFC--TDMD-RRGD 304
Qy 356 FRILMCTKVMTDDFLTAHEMGGH-IQYDMAYAAQPFLLRNGANEGPHEAVGIMSLSAT 414
Db 305 IRVLLNDQSMYVWTALLHEFGHAVYFKFDISRLPELLR-----PH-----SHTLTT 351
Qy 415 PRHLKSIGLLS--PDFOE-----DNET-----EINFLKQALTIIVTLPFTYMLEKRW 461
Db 352 EASALPFGMTKNAEYVERPLGDRDTCRIGRMMEKMLQRM-VVST-----RW 400
Qy 462 MV-----FKG---BIPQDMKKMKWEMKREIVGVVPHDETYCDPASLFHVS-----N 508
Db 401 MLAFSPFKSLYEDPDQDINALMWKLVIQYMAP--PEDTGSDDWAAKWHFLAPVYVO 458
Qy 509 DY-----SFIRYVTRT 519
Db 459 DYLLEMAASQLHYIKT 476

RESULT 15
AF1310
probable thermostable carboxypeptidases homolog lmo1886 [imported] - Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AF1310
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative Genomics of Listeria species
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AF1310
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-502 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC99964.1; PID:g16411339; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Gene: lmo1886
C;Superfamily: Thermus aquaticus carboxypeptidase Taq

Query Match 3.6%; Score 154; DB 2; Length 502;
Best Local Similarity 20.1%; Pred. No. 0.0085;
Matches 128; Conservative 101; Mismatches 215; Indels 192; Gaps 35;

Qy 20 TIEQAKTFLLDKFNHEADLPYQSSLASWNYNT-----NITEENVQNNNA 65
Db 4 TLEEFLLAYIKKMEALSEAL---ALVYVDLRTGAPAKMGESRSDVIGVLSSEIFNNQTS 59
Qy 66 GDKWSAFLKEOSTLAQMYPLQEIQNLTKLQALQONGSSVLSSEDSKSL-----N 117
Db 60 -EEMAAFIAGLN-----QDKENLS-EITRKTLEE---SQKTYDLNKKIPSKYAEYT 106
Qy 118 TILNTMTIYSTGKVCNPDNPQECLELLEPGNEIMANSLDYNERLWAWESWRSEVQKLR 177
Db 107 KLVAQAEATAWTAREQN-----DFAAFEPFLTKIL-----136
Qy 178 PLYEYVVLKNEMARANHVEDYDWRGDEYVNGVDGY--DYSRGQLIEDVHTEFIKIP 235
Db 137 -----EMKR-----KFVEYV--GYEENKYDILLDQYEPGVTVSVLDSVFEKVR- 177
Qy 236 LYEHLHAYVRAKLNNAYPSYISPIGCLPAHLGDMWGRFTNLYSLTVFPQCKPNIDVTD 295
Db 178 --DGIMA-IREKIENE-----GVKPDATILN 200
Qy 296 AMVDQAWDAQRIKFAEKFEVSVGLPNTQGFWENSLTDPGNVQKAVCHPTAMDGLKGD 355
Db 201 TKISEA-----KQKEFSIRI-LNKGDFD-----EAGRLDET-V-HFPAIATGLNTGD 243
Qy 356 PRILMCTKVMTDDFLTA-----HHEMGHIQY-----DMAYAAQPFLLRNGANEGPHEAVG-- 405

Search completed: February 19, 2004, 19:51:41
Job time : 25 secs

Db 244 VRI--TTRYNENDFKMAVFGTIHEGGHAIYEQNFDAALVGTP--LANGASMGIHESQSLF 299
Qy 406 -EIM--SLSAATPKHLKSTIGLLSPDFQ-----ED-----NETEINFLKQALTIIVGTLP- 451
Db 300 YEIIIGSSLAFWKSNYADFOAITKPAFDQVKLEDFYRAVNISESSLIRIEADTL--TYPL 357
Qy 452 ---FTYMLEKRWVFKGBIPKQWMMKQWEMKREIVGVVPEVPHDETYCDPASLFHVS 508
Db 358 HIMIRYELEK---ALINGELEVKDLPKAWGDKVEEYLG---RPDNDTNGVLOQDIHWAGG 411
Qy 509 DYSFIRYVTRT-LYQFOFQBALCOAAKHEGLHKDCISNSTEAGQKLF---NMLRLGKSE 564
Db 412 DFGYFPPSYALCLMYAAQFFNQW-----QKEIPNIDAIIASDDYSELKIMLIEHVHKEGKTK 467
Qy 565 PWTALENVVGAKNNVRPLINYPEPLFTWLKQONK 600
Db 468 KPLEILDTTTC-EGLNPTYLLDLLEKRYAYVYQFNK 502

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 19, 2004, 19:44:13 ; Search time 17 Seconds
(without alignments)
2226.853 Million cell updates/sec

Title: US-09-163-648-2

Perfect score: 4291

Sequence: 1 MSSSSWLLSLVAVTAAQST.....ISKGNPFQNTDDVQSF 805

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1344	31.3	732	1 ACET_HUMAN	P22966 homo sapien
2	1337	31.2	1306	1 ACE_HUMAN	P12821 homo sapien
3	1334	31.1	732	1 ACET_MOUSE	P22967 mus musculus
4	1334	31.1	1312	1 ACE_MOUSE	P09470 mus musculus
5	1312	30.6	1193	1 ACE_CHICK	Q10751 gallus gall
6	1310	30.5	1313	1 ACE_RAT	P47820 rattus norv
7	1283.5	29.9	1310	1 ACE_RABIT	P12822 coryctolagus
8	1283	29.9	737	1 ACET_RABIT	P22968 coryctolagus
9	1085	25.3	615	1 ACE_DROME	Q10714 drosophila
10	1058	24.7	611	1 ACE_HAIE	Q10715 haematobia
11	135	3.1	501	1 YPWA_BACSU	P50848 bacillus su
12	125	2.9	627	1 GLGB_BACSU	P39118 bacillus su
13	123	2.9	986	1 EP1B_STABP	P30195 staphylococ
14	121	2.8	1034	1 BGAL_BACME	O52847 bacillus me
15	119.5	2.8	1283	1 OSH2_YEAST	Q12451 saccharomyc
16	119.5	2.8	3655	1 YAMB_SCHPO	Q10064 schizosacch
17	119.5	2.8	4540	1 DYHC_PART	Q27171 paramesum
18	118	2.7	663	1 MTHR_CABEL	Q17693 caenorhabdi
19	118	2.7	1826	1 K13B_HUMAN	Q9ngt8 homo sapien
20	118	2.7	3911	1 AXA9_HUMAN	Q99996 h a-kinase
21	115.5	2.7	3433	1 UTR9_HUMAN	P46939 homo sapien
22	115	2.7	950	1 Y511_RICPR	Q9zd36 rickettsia
23	114.5	2.7	901	1 PIP_LACLA	P49022 lactococcus
24	114.5	2.7	1225	1 Y309_MYCGE	P47551 mycoplasma
25	114	2.7	1284	1 CWFB_SCHPO	O94508 schizosacch
26	113.5	2.6	6669	1 NEBU_HUMAN	P20929 homo sapien
27	113	2.6	638	1 SYM_THETN	Q8rd01 thermocoaer
28	113	2.6	6885	1 SNE2_HUMAN	Q8wxh0 homo sapien
29	112.5	2.6	773	1 CDH_FHACH	Q01738 phanerocha
30	112.5	2.6	782	1 OSTA_PASNU	Q9ck12 pasteurella
31	110	2.6	660	1 SYN_BACHD	Q9kgk8 bacillus ha
32	109.5	2.6	1398	1 DNA2_SCHPO	Q9uruz schizosacch
33	109	2.5	906	1 Y010_CLOAB	Q97n28 clostridium

ALIGNMENTS

RESULT 1

ACET_HUMAN
ID ACET_HUMAN STANDARD; PRT; 732 AA.
AC P22966;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Angiotensin-converting enzyme, testis-specific isoform precursor
DE (EC 3.4.15.1) (ACE-T) (Dipeptidyl carboxypeptidase I) (Kininase II).
GN ACE OR DCP1 OR DCP
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90046671; PubMed=2554286;
RA Ehlers M.R.W., Fox E.A., Strydom D.J., Riordan J.P.;
RT "Molecular cloning of human testicular angiotensin-converting enzyme;
RT the testis isozyme is identical to the C-terminal half of endothelial
RT angiotensin-converting enzyme.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:7741-7745 (1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89338720; PubMed=2547653;
RA Lattion A.D., Soubrier F., Allegrini J., Hubert C., Corvol P.,
RA Alhenc-Gelas F.;
RT "The testicular transcript of the angiotensin I-converting enzyme
RT encodes for the ancestral, non-duplicated form of the enzyme.";
RL FEBS Lett. 252:99-104 (1989).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS PRO-32; GLY-49 AND SER-712.
RX MEDLINE=99251580; PubMed=10319862;
RA Rieder M.J., Taylor S.L., Clark A.G., Nickerson D.A.;
RT "Sequence variation in the human angiotensin converting enzyme.";
RL Nat. Genet. 22:59-62 (1999).
RN [4]
RP ZINC-BINDING.
RX MEDLINE=91308093; PubMed=1649623;
RA Ehlers M.R., Riordan J.P.;
RT "Angiotensin-converting enzyme: zinc- and inhibitor-binding
RT stoichiometries of the somatic and testis isozymes.";
RL Biochemistry 30:7118-7126 (1991).
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE=96302256; PubMed=8755737;
RA Sturrock E.D., Yu X.C., Wu Z., Biemann K., Riordan J.P.;
RT "Assignment of free and disulfide-bonded cysteine residues in testis
RT angiotensin-converting enzyme: functional implications.";
RL Biochemistry 35:9560-9566 (1996).
CC -!- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF
CC THE TERMINAL HIS-LEU. THIS RESULTS IN AN INCREASE OF THE
CC VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN. ALSO ABLE TO INACTIVATE
CC BRADYKININ, A POTENT VASODILATOR.
CC -!- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,
CC oligopeptide-|-Xaa-Xbb, when Xaa is not Pro, and Xbb is neither

34 108.5 2.5 1084 1 XPO1_YEAST P30822 saccharomyc
35 108.5 2.5 2167 1 BP11_YEAST P25356 saccharomyc
36 107.5 2.5 1689 1 RPAL_SCHPO P15398 schizosacch
37 107.5 2.5 3685 1 DMD_HUMAN P11532 homo sapien
38 107 2.5 736 1 VE4_ROTFC P26193 porcine rot
39 106.5 2.5 1312 1 PASO_YEAST P12753 saccharomyc
40 106.5 2.5 1499 1 RHGS_HUMAN Q13017 homo sapien
41 106 2.5 1279 1 BCHH_CHLVI OS0314 chlorobium
42 105.5 2.5 645 1 REP_BUCAI P57654 buchnera ap
43 105.5 2.5 1002 1 POL_HV1U4 P24740 human immun
44 105 2.4 626 1 HTPG_BUCBP Q89a93 buchnera ap
45 104.5 2.4 757 1 2A5D_YEAST P38903 saccharomyc

Asp nor Glu. Converts angiotensin I to angiotensin II.
-!- COFACTOR: Binds 1 zinc ion (by similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=Testis-specific;
IsoId=22966-1; Sequence=Displayed;
Name=Somatic;
IsoId=21821-1; Sequence=External;
-!- TISSUE SPECIFICITY: SPERMATOCYTES, ADULT TESTIS.
-!- INDUCTION: EXPRESSION IS THOUGHT TO BE SUBJECT TO HORMONAL
REGULATION BY ANDROGENS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
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or send an email to license@isb-sib.ch).
EMBL; M26657; AA060611.1; -;
EMBL; X16295; CA34362.1; -;
EMBL; AF118569; AAD28561.1; -;
PIR; S05238; S05238.
MEROPS; M02.004; -;
Genew; HGNC:2707; ACE.
MIM; 106180; -;
GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0004245; P:peptidyl-dipeptidase A activity; TAS.
GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
InterPro; IPR001548; Peptidase M2.
Pfam; PF01401; Peptidase M2; 1.
PRINTS; PR00791; Peptidase M2.
ProDom; PD004184; Peptidase M2; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;
KW Glycoprotein; Transmembrane; Testis; Signal; Alternative splicing;
KW Polymorphism.
FT SIGNAL 1 31 ANGIOTENSIN-CONVERTING ENZYME, TESTIS-
FT CHAIN 32 732 SPECIFIC ISOFORM.
FT DOMAIN 32 684 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 685 701 POTENTIAL.
FT DOMAIN 702 732 CYTOPLASMIC (POTENTIAL).
FT METAL 414 414 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT SITE 415 415 BY SIMILARITY.
FT METAL 418 418 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 442 442 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT SITE 457 457 POTENTIAL.
FT DISULFID 183 189
FT DISULFID 383 401
FT DISULFID 569 581
FT CARBOHYD 103 103
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 617 617 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 32 32 S -> P (IN dBSNP:4317).
FT VARIANT 49 49 S -> G (IN dBSNP:4318).
FT VARIANT 444 444 I -> T (IN dBSNP:4976).
FT VARIANT 477 477 P -> V (IN dBSNP:4977).
FT VARIANT 705 705 R -> Q (IN dBSNP:4980).
FT VARIANT 712 712 R -> S (IN dBSNP:4364).
FT VARIANT 712 712 /FTId=VAR_011712.

FT VARIANT 722 722 Q -> P (IN dBSNP:4981).
FT /FTId=VAR_014741.
SQ SEQUENCE 732 AA; 83330 MW; 80E0D19CFA642313 CRC64;
Query Match 31.3%; Score 1344; DB 1; Length 732;
Best Local Similarity 41.8%; Pred. No. 8.4e-87;
Matches 259; Conservative 119; Mismatches 204; Indels 38; Gaps 10;
QY 15 TAAQS-----TIEQAKTFLDFXHEAEDLFYQSSLASNNYNTITE-----NQVM 62
DB 61 TSAQSPNLVTDEAEASKVEYDRTSQVWMEYAEANNYNTITTTSTSKLLQKNQIA 120
QY 63 NNAGDKSAFLKEQSTLAQYPLQEIQLTVKLOALQQSGSVLSSEDKSKRLNTILNT 122
DB 121 NHT-----LKYGTQARKFDVQLOQNTIIRIKKVDLERALPAQELBEYNKILLD 172
QY 123 MTTIYSTGVKNPDNPQRCLELLEPGLEINEMANSIDYNERLWMSRSEVQKQIRPLYEE 182
DB 173 MTTTYSVATVCHPNG--SCLQLEPDLTNVMTSRKYEDLLWAWEGWRDKAGRAILQFYPK 230
QY 183 YVVLKNEVARAHNYEDYDGYWRGDEYVNGVDGYDSRQLIEDVEHTFEEIKPLYEHLHA 242
DB 231 YVELINQAARLNGYVDAGSMRSMTYETPSLE-----CDLERLFOELQPLYNLHA 280
QY 243 YVRAKIMNAY-PSYISPIGCLPAHLLGDMWGRFNTLYSLVPPFOGXPNIDVTDAMVQA 301
DB 281 YVRRALHRYGAQHINLEGPISAHLLGNWAGTWSNIYDLVVPFSPASPSMDTTEAMLKQG 340
QY 302 WDAQRIFKEAEKFFVSVGLPNMTQCFWNSMLTDGPNQKAVCHPTAMDLGKG-DRIILM 360
DB 341 WTPRRMKFKAADDFTSLGLLPVPPEFWNKSMLEKPTDGRVGVVCHASANDFYNGKDFRIKQ 400
QY 361 CTXVTMDDELTAHHEMGHIQYDMAYAAAPFLLRNGANEGFHEAVGEIMSLSAATPKLHS 420
DB 401 CTYVNLDELVAHHEMGHIQYFMQYKDLFVALREGANPGFHEAIGDVLALSVPKHLHS 460
QY 421 IGLLSPDFQEDNETEINFLKQALITVGLTPFTYMLEKRWNVFKGEIPKQDMKKWEM 480
DB 461 LNLSSGEGSD-EHDINFLMKALDKIAFIPFSYLVQDMRWVFDGSIKTENYNQEWNSL 519
QY 481 KRIIVGVSPVPHDETYCPASLHFVSNDSYIRYVTRTYQFQFQFQFQFQFQFQFQF 540
DB 520 RLKYQGLCPVPTQDFFPGAKFHPSPVIRYFVSFIIQFQFHEALCQAAGHTGPLH 579
QY 541 KCDISNSTEAGQKLFNNMLRGKSEPTWLALENVVGANQNNVPLLYFPPLFTWLKQNK 600
DB 580 KCDIYQSKAGORLATAMKLGFSRPWPEANQLITQPNMSASAMLSYFKPLDLDWLTENE 639
QY 601 --NSFCGW-STDWSPVADOS 617
DB 640 LHGEKLGWPOYNWIPNSARS 659
RESULT 2
ACE_HUMAN STANDARD; PRT; 1306 AA.
ID ACE_HUMAN
AC P12821, 1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, last sequence update)
DT 01-OCT-1989 (Rel. 12, last annotation update)
DT 28-FEB-2003 (Rel. 41, last annotation update)
DE Angiotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1)
DE (ACE) (Dipeptidyl carboxypeptidase I) (Kinase II) (CD143 antigen).
DE ACE OR DCP1 OR DCP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
EX MEDLINE=89071703; PubMed=2849100;
RA Soubrier F., Allenc-Gelas F., Hubert C., Allegrini J., John M.,
RA Tregear G., Corbol P.;
RA "Two putative active centers in human angiotensin I-converting enzyme

RT revealed by molecular cloning.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:9386-9390 (1988).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANTS SER-261; TRP-561 AND SER-1286.
 RA MEDLINE=9251580; PubMed=10319862;
 RX Rieder M.J., Taylor S.L., Clark A.G., Nickerson D.A.;
 RL "Sequence variation in the human angiotensin converting enzyme.";
 RT Nat. Genet. 22:59-62 (1999).
 RN [3]
 RP PARTIAL SEQUENCE OF 30-46.
 RC TISSUE=Lung;
 RX MEDLINE=90110025; PubMed=2558109;
 RA Takeuchi K., Shimizu T., Ohishi N., Seyama Y., Takaku F.,
 RN Yotsumoto H.;
 RT "Purification of human lung angiotensin-converting enzyme by high-performance liquid chromatography: properties and N-terminal amino acid sequence.";
 RL J. Biochem. 106:442-445 (1989).
 RN [4]
 RP ZINC-BINDING.
 RX MEDLINE=91308093; PubMed=1649623;
 RA Ehlers M.R., Riordan J.F.;
 RT "Angiotensin-converting enzyme: zinc- and inhibitor-binding stoichiometries of the somatic and testis isozymes.";
 RL Biochemistry 30:7118-7126 (1991).
 RN [5]
 RP VARIANTS THR-1018; VAL-1051; GLN-1279; SER-1286 AND PRO-1296.
 RX MEDLINE=99318094; PubMed=10391210;
 RA Halushka M.K., Fan J.-B., Bentley K., Haie L., Shen N., Weder A.,
 RN Cooper R., Lipshutz R., Chakravarti A.;
 RT "Patterns of single-nucleotide polymorphisms in candidate genes for blood-pressure homeostasis.";
 RL Nat. Genet. 22:239-247 (1999).
 CC -!- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF THE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF THE VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN. ALSO ABLE TO INACTIVATE BRADYKININ A POTENT VASODILATOR.
 CC -!- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide.
 CC oligopeptide--|-Xaa-Xbb, when Xaa is not Pro, and Xbb is neither Asp nor Glu. Converts angiotensin I to angiotensin II.
 CC -!- COPACITOR: Binds 2 zinc ions (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=Somatic;
 CC IsoId=PI2821-1; Sequence=Displayed;
 CC Name=Testis-specific;
 CC IsoId=P22966-1; Sequence=External;
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
 CC -!- DATABASE: NAME=PRO; NOTE=CD guide CD143 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd143.htm".
 CC -----
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 CC -----
 CC EMBL; J04144; AA051684.1; -;
 CC EMBL; AF118569; AA028560.1; -;
 CC PIR; A31759; A31759.
 CC MEROPS; M02.001; -;
 CC MEROPS; M02.004; -;
 CC Genew; HGNC:2707; ACE.
 CC MIM; 106180; -;
 CC GO; GO:0005624; C:membrane fraction; TAS.
 CC GO; GO:0005886; C:plasma membrane; TAS.
 CC GO; GO:0005625; C:soluble fraction; TAS.
 CC GO; GO:0008217; P:regulation of blood pressure; TAS.
 CC InterPro; IPR001548; Peptidase_M2.
 CC InterPro; IPR006025; Zn_MTPeptide.

DR PFam: PF01401; Peptidase M2; 2.
 DR PRINTS; PR00791; PEPTIDPASE.
 DR PRODom; PD004184; Peptidase M2; 2.
 DR PROSITE; PS00142; ZINC_PROTEASE; 2.
 KW Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;
 KW Glycoprotein; Transmembrane; Repeat; Signal; Alternative splicing;
 KW Polymorphism.
 FT SIGNAL 1 29 ANGIOTENSIN-CONVERTING ENZYME, SOMATIC
 FT CHAIN 30 1306 ISOFORM.
 FT DOMAIN 30 1259 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1260 1276 POTENTIAL.
 FT DOMAIN 1277 1306 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 227 583
 FT REPEAT 825 1181
 FT METAL 390 390
 FT ACT SITE 391 391 ZINC 1 (CATALYTIC) (BY SIMILARITY).
 FT METAL 394 394 ZINC 1 (CATALYTIC) (BY SIMILARITY).
 FT METAL 988 988 ZINC 2 (CATALYTIC) (BY SIMILARITY).
 FT ACT SITE 989 989 ZINC 2 (BY SIMILARITY).
 FT METAL 992 992 ZINC 2 (CATALYTIC) (BY SIMILARITY).
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 74 74 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 111 111 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 272 272 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 318 318 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 445 445 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 509 509 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 677 677 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 695 695 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 714 714 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 760 760 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 942 942 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1191 1191 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARIANT 261 261 A -> S.
 FT VARIANT 561 561 R -> W.
 FT VARIANT 1018 1018 /FTID=VAR_011708.
 FT VARIANT 1051 1051 I -> T (IN dBSNP:4976).
 FT VARIANT 1051 1051 F -> V (IN dBSNP:4977).
 FT VARIANT 1279 1279 /FTID=VAR_014190.
 FT VARIANT 1286 1286 R -> Q (IN dBSNP:4980).
 FT VARIANT 1296 1296 /FTID=VAR_014191.
 FT VARIANT 1296 1296 R -> S (IN dBSNP:4364).
 FT VARIANT 1296 1296 Q -> P (IN dBSNP:4981).
 FT VARIANT 1296 1296 /FTID=VAR_014192.
 FT CONFLICT 35 35 O -> E (IN REF. 2).
 FT CONFLICT 42 42 D -> R (IN REF. 2).
 SQ SEQUENCE 1306 AA; 149714 MW; 1B39BCA301A268A CRC64;
 Query Match 31.2%; Score 1337; DB 1; Length 1306;
 Best Local Similarity 41.7%; Pred. No. 6.1e-86;
 Matches 255; Conservative 118; Mismatches 204; Indels 34; Gaps 9;
 QY 20 TIEQAKTFLDKENHEAEDLFYQSSIASWYNTNTEE-----NVQNMNAGDKWSA 71
 DB 644 TDEAEASKFVEEYDRTSQVWNEAYANWYNTNITETSKILLQKNQIAHNT----- 697
 QY 72 FLKEQSTLAQMPLOEIQNLTKVLQLOALQONGSSVLSEDKSKRLNTILNTWTISTYSTOK 131
 DB 698 --LKYGTQARKFDVNQLQNTTKRIKKYQDLERAAALPAQELEYVKNILLDMETTVSVAT 755
 QY 132 VCNPDNPQECILLLEPGINIMANSLDNERLWAWESWRSEVGKQLRPLVEYVWLKNWA 191
 DB 756 VCHENG--SCLQLEPDLTNWMTATSKRYEDLLWAWEGWRDKAGRAILOFTPKEVELINQA 813
 QY 192 RANHYEDYGDYWRGDEYVNGVDYSGRLIEDVEHTFEIKPLYEHLHAYVRKLMNA 251


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Db 814 RLNGYVDAGDSWMSYETPSLE-----ODLERFQELQPLYLNLHAYVZRALHRH 863
Qy 252 Y-PSYISPIGCLPAHLGLGDMGKGFNTNLSLVPFQKPNIDVTDAMVDQAWDAQRIFKE 310
Db 864 YGAQHINLEGPIDAHLLGNNAWQTSNIYDLVPPFAPSMDTTEAMLKQGTWTRWFKE 923
Qy 311 AEKFFSVGLPNNTOGFWNSMLTDGNTOKAVCHPTAWDLGK-DEPILACTVMTDDF 369
Db 924 ADDFFSLGLPVPFPPFNKSMLEKETDGREVVVCASAWDFYNGKDFRIKCTTNNLEDL 983
Qy 370 LTAHEHGHIIQYDVAAYAAOFFLLRNGANGFHEAVEGMSLSAATPKLKSIGLLSPDFQ 429
Db 984 VWAHEHGHIIQYDVAAYAAOFFLLRNGANGFHEAVEGMSLSAATPKLKSIGLLSPDFQ 1043
Qy 430 EDNETETNPLKALATVGLPTPTMEXRWVFKGEIPKDDKMKWEMKREIVGVVE 489
Db 1044 SD-EHDINFLMKVALDKIAFIPSYLVQWRVRVFGSTIKENYQEWWSRLKVKGLCP 1102
Qy 490 PVHDEPYCDPASLHVNSNDYSIRYTRTLVQFOFQEQALCOAAKHGFLHKDISNSTE 549
Db 1103 PVHRTQDFGFAKFIHPSVPYIRYFVSFIQFOFHEALCOAAHGTGFLHKCDIYOSKE 1162
Qy 550 AGOKLFNMLRLGKSEPTWLTALENVGAKMNVRLPLNYFPELFTWLKDKNK-NSFVGV- 606
Db 1163 AGORLATAMKLGSRPWPANQILITQPNWSASAMLSYFKPLLDLWLTENELHGEKLGWP 1222
Qy 607 STWSPVADOS 617
Db 1223 QYNWTFNSARS 1233

RESULT 3
ACET_MOUSE STANDARD; PRT; 732 AA.
ID ACET_MOUSE
AC P22967;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Angiotensin-converting enzyme, testis-specific isoform precursor
DE EC 3.4.15.1 (ACE-T) (Dipeptidyl carboxypeptidase I) (Kinase II).
GN ACE OR DCP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90318396; PubMed=2164636;
RA Howard T.E., Shai S.-Y., Langford K.G., Martin B.M., Bernstein K.E.;
RT "Transcription of testicular angiotensin-converting enzyme (ACE) is
RL initiated within the 12th intron of the somatic ACE gene.";
RL Mol. Cell. Biol. 10:4294-4302(1990).
CC -1- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF
CC THE TERMINAL HIS-LEU. THIS RESULTS IN AN INCREASE OF THE
CC VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN.
CC -1- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,
CC oligopeptide.-|-Xaa-Xbb, when Xaa is not Pro, and Xbb is neither
CC Asp nor Glu. Converts angiotensin I to angiotensin II.
CC -1- COFACTOR: Binds 1 zinc ion (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Testis-specific;
CC IsoId=P22967-1; Sequence=Displayed;
CC Name=Somatic;
CC IsoId=P09470-1; Sequence=External;
CC -1- TISSUE SPECIFICITY: SPERMATOCYTES, ADULT TESTIS.
CC -1- INDUCTION: EXPRESSION IS THOUGHT TO BE SUBJECT TO HORMONAL
CC REGULATION BY ANDROGENS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M55333; AAA37149.1; -.
DR EMBL; M61094; AAA37150.1; -.
DR PIR; A35655; A35655.
DR MEROPS; M02.004; -.
DR MGD; MGI:87874; Ace.
DR InterPro; IPR001548; Peptidase M2.
DR InterPro; IPR006025; Zn_Mtpptdse.
DR Pfam; PF01401; Peptidase M2; 1.
DR PRINTS; PR00791; PEPTIDASEA.
DR ProDom; PD004184; Peptidase M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;
KW Glycoprotein; Transmembrane; Testis; Signal; Alternative splicing.
FT SIGNAL 1 31
FT CHAIN 32 732
FT ANGIOTENSIN-CONVERTING ENZYME, TESTIS-
FT SPECIFIC ISOFORM.
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 32 684
FT TRANSMEM 685 701
FT DOMAIN 702 732
FT METAL 413 413
FT ACT_SITE 414 414
FT METAL 417 417
FT METAL 441 441
FT DISULFID 182 188
FT DISULFID 382 400
FT DISULFID 568 580
FT CARBOHYD 102 102
FT CARBOHYD 120 120
FT CARBOHYD 139 139
FT CARBOHYD 185 185
FT CARBOHYD 367 367
FT CARBOHYD 616 616
SQ SEQUENCE 732 AA; 80407 MW; 16C817E7FBD09BD9 CRC64;

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Query Match 31.1%; Score 1334; DB 1; Length 732;

Best Local Similarity 42.6%; Pred. No. 4.3e-86;

Matches 255; Conservative 112; Mismatches 213; Indels 18; Gaps 7;

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Qy 20 TTEQAKTFLDKFNHEADLFYQSSLASWNTNTITEVONMNNAGDKWSAFLEKQSTL 79
Db 69 TDEAKADRFVEYDRTAQVLLNEAYEANWQNTITTEGSKILLEKSTESVNHLYKGT 128
Qy 80 AQMPYPLQEIQLTVKLOLQALQONGSSVLSEDKSKRLNTINTMTSTIYSTGKVCNPDNPQ 139
Db 129 AKTFDVSNFQSSIKRIKKLQNLDRVLPPKELEYNQILLDMETTSYLSNICYNG-- 186
Qy 140 ECLLEPGLNEYMANSLDYNERLWAWESWRSEVKQRLPYEEVTVLKEMANAHVEDY 199
Db 187 TCMLEPDLTNMATSRYKIELLWAWKSRDKVGRALPPFPFKYVESNKIAKLNGYDA 246
Qy 200 GYWRGDYEVNGVDGYDSRGQLEDEVEHTEPEIKPLYEHLHAYVRKAKLMNAPYS-YISP 258
Db 247 GDSWRSLYESDNL-----QDLEKLYOELQPLYLNLHAYVRSRHRHYSYINL 296
Qy 259 IGCLPAHLGLGDMGKGFNTNLSLVPFQKPNIDVTDAMVDQAWDAQRIFKEKPFVS 318
Db 297 DGFIPAHLLGNNAWQTSNIYDLVPPFAPSMDTTEAMLKQGTWTRWFKEADNFTSL 356
Qy 319 GLPNNTOGFWNSMLTDGNTOKAVCHPTAWDLGK-DFRILMCTKVTMDDFLTAHEMG 377
Db 357 GLLPVPFPPFNKSMLEKETDGREVVVCASAWDFYNGKDFRIKQCTSVNMEDLVIAHEMG 416
Qy 378 HICYDVAAYAAOFFLLRNGANGFHEAVEGMSLSAATPKLKSIGLLSPDFQEDNETEIN 437
Db 417 HICQFMQYKDLVPTFREGANFGFHEAIGDIMALSVSTPKHLYSLNLLSTE-GSGYEYDIN 475

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QY 498 CDPASLFHVSNDYSFIRYTRTLTYQFOFQOEALCOAAKHEGLHKKCDISNSTRAGOKLFNM 557
DB 1116 FDPGSKHVPANVYFVYFVFIQFOFHEALCRAAGTGLPKCDIYQSKAGKLIADA 1175
QY 558 LRLKSPPTLALENVVGAKNMVRPLNYPFELFTWLKQDNK--NSFVGM-STDWSP 612
DB 1176 MKLGYSKPWPEAMKLIITGQPNNSASAMNYPKPLTEMLVTENRRHGETLGNWPEYNWAP 1233
RESULT 5
ACE_CHICK STANDARD; PRT; 1193 AA.
ID _ACE_CHICK
AC Q10751;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiotensin-converting enzyme (EC 3.4.15.1) (Dipeptidyl
carboxypeptidase I) (Kininase II) (Fragment).
GN ACE OR DCPI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=95110342; PubMed=7811282;
RA Esther C.R., Thomas K.E., Bernstein K.E.;
RT "Chicken lacks the testis specific isozyme of angiotensin converting
enzyme found in mammals."
RL Biochem. Biophys. Res. Commun. 205:1916-1921(1994).
CC THE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF
VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN
CC -! CATALYTIC ACTIVITY: Release of a C-terminal dipeptide
oligopeptide--|-Xaa-Xbb, when Xaa is not Pro, and Xbb is neither
Asp nor Glu. Converts angiotensin I to angiotensin II.
CC -! COFACTOR: Binds 2 zinc ions (By similarity).
CC -! SUBCELLULAR LOCATION: Type I membrane protein.
CC -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L40175; AAA5554.1; -;
CC PIR; JC2489; JC2489.
CC MEROPS; M02.001; -;
CC InterPro; IPR001548; Peptidase_M2.
CC InterPro; IPR006025; Zn_MTPeptide.
CC Pfam; PF01401; Peptidase_M2; 2.
CC PRINTS; PR00791; PEPDPTASEA.
CC ProDom; PD004184; Peptidase_M2; 2.
CC PROSITE; PS00142; ZINC_PROTEASE; 2.
CC KEGG; K01142; Zinc protease; Zinc; Dipeptidase;
KW Hydrolase; Metalloprotease; Carboxypeptidase; Repeat.
KW Glycoprotein; Transmembrane; Repeat.
FT NON_TER 1 1 EXTRACELLULAR (POTENTIAL).
FT DOMAIN <1 1156 POTENTIAL.
FT TRANSMEM 1157 1173 POTENTIAL.
FT DOMAIN 1174 1193 CYTOPLASMIC (POTENTIAL).
FT REPEAT 125 481
FT REPEAT 723 1079
FT METAL 288 288
FT ACT_SITE 289 289
FT METAL 292 292
FT METAL 886 886
FT ACT_SITE 887 887
ZINC 1 (CATALYTIC) (BY SIMILARITY).
1 (BY SIMILARITY).
ZINC 1 (CATALYTIC) (BY SIMILARITY).
ZINC 2 (CATALYTIC) (BY SIMILARITY).
2 (BY SIMILARITY).

FT METAL 890 890 ZINC 2 (CATALYTIC) (BY SIMILARITY).
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 407 407 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 485 485 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 513 513 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 555 555 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 575 575 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 658 658 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1089 1089 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1193 AA; 137820 MW; 954472A18EA471C7 CRC64;
Query Match 30.6%; Score 1312; DB 1; Length 1193;
Best Local Similarity 40.4%; Pred. No. 3.1e-84;
Matches 264; Conservative 110; Mismatches 243; Indels 36; Gaps 10;
QY 22 BEQAKTFLDKFNHEADLPYQSSLASWNYNTNITENVNMMNAGDKWSAFLEKQSTLAAO 81
DB 544 EAQAKFLESEYNSTAEVVMNAYTEASWEYNTNITDHNKEVLMLEKRLAMSKHTIEYGMAR 603
QY 82 MYPLOEQNLTVKLOLQALQQNGSSVLSEDKSKRLNTILNTMTSTIYTGKVCNPN--P 138
DB 604 QFDPSPQDETTRINKLSVLERAALPEDELKEYNTLLSDMETTYSVAKVCRENNTFR 663
QY 139 QECILLEPGNLIMANSLDYNERLWAWSRSEVQKQLRPLYEYVVLKNEVARAHYED 198
DB 664 -----LDPDLTDILATSRDYNELLFAWKGWWDASAKIKDKYKRYVELSKAAVLNGYD 718
QY 199 YGDYMGDYGNGVDGYDSRQQLTEVDHTEPEELKPLYEHLHAYVRAKLINAY-PSYIS 257
DB 719 NGAYWASLLETPTFE-----EDLELYLQQLYPLNLHAYVRRALYKNGYAEHIS 768
QY 258 PIGCLPAHLGLDMGFRWNTLYSLTVFQCKNIDVTDAMVDQAWDAQRIKFAEAEKFFVS 317
DB 769 LKGPIDPAHLGLNMAQSNIFDLVMPFPDPAKVDATPAKQOGWTPKXMFESDRFFTS 828
QY 318 VGLPNNTQGFWSMLTDQNTQKAVCHPTAMD--GKGFRLIMCTKVMTDDFLTAHHEM 376
DB 829 LGIIPMPQEFWDKSMTEKFAADREVVCCHASANDFYNRKDFRIKQCTVVMDDLLITVHEM 888
QY 377 GHIQYDMAYAAQPFLLRNGANEGFHAAGVIEIMSLSAATPKHLKSGILLSPDQEDNETEI 436
DB 889 GHVQYFLQYMDQPISPFDGANPGFHAIGDVMALSSTPKHLHSINLLD-QVTNEESDI 947
QY 437 NFKLKQALTIVGTLPTMYLKKRWVVFGEIPKQDMKKWEMKREIVGVVPEVPHDET 496
DB 948 NYLMSIALDKIAFLPFGYLMQWRKVFDRKEDYEQWNLRLKYQGLCPPVERSED 1007
QY 497 YCDPASLFHVSNDYSFIRYTRTLTYQFOFQOEALCOAAKHEGLHKKCDISNSTRAGOKLFN 556
DB 1008 DFDPGAKFHIPANVYFVYFVFIQFOFHEALCRAAGTGLPKCDIYQSKAGKLIAD 1067
QY 557 MLRLKSPPTLALENVVGAKNMVRPLNYPFELFTWLKQDNK--NSFVGM-STDWSPY 613
DB 1068 AMKLFGSKPWPEAMKLIITGQPNNSAALMSYFPELMTLVKQKTENGEVLGNWPEYNTPY 1127
QY 614 ADQSIKVRISLKSALG-----DKAYEMNDNEMYLFRSSVAYAMQYFLKVK 659
DB 1128 AVTEFHAATDADFLGNSVGTGKQATAGAW-----VLLALAVELITSIFLGVK 1175
RESULT 6
ACE_RAT
ID _ACE_RAT
AC P47820; STANDARD; PRT; 1313 AA.
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1)
DE (ACE) (Dipeptidyl carboxypeptidase I) (Kininase II).
GN ACE OR DCPI.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=94121659; PubMed=8292044;
RA Koike G., Krieger J.E., Jacob H.J., Mukoyama M., Pratt R.E.,
RA D'au V.J.;
RA "Angiotensin converting enzyme and genetic hypertension: cloning of
RT rat cDNAs and characterization of the enzyme";
RL Biochem. Biophys. Res. Commun. 198;380-386(1994).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=Lewis/N; TISSUE=Lung;
RA Jafarian-Tehrani M., Listwak S., Barrientos R.M., Michaud A.,
RA Corvol P., Sternberg E.M.;
RA "Characterization of a missense mutation in the angiotensin
RT I-converting enzyme cDNA in exudative inflammation resistant F344/N
RT rats";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF
CC THE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF THE
CC VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN.
CC -!- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,
CC oligopeptide-Xaa-Xbb, when Xaa is not Pro, and Xbb is neither
CC Asp nor Glu. Converts angiotensin I to angiotensin II.
CC -!- COFACTOR: Binds 2 zinc ions (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Somatic;
CC IsoId=P47820-1; Sequence=Displayed;
CC Name=Testis-specific;
CC IsoId=P47820-2; Sequence=Not described;
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
CC
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CC or send an email to license@ebi.ac.uk).
CC
CC EMBL: U03708; AAA82110.1; -;
CC EMBL: U03734; AAA82111.1; -;
CC EMBL: AF201332; AAC35597.1; -;
CC PIR: JC2038; JC2038.
CC MEROPS: M02.001; -;
CC INTERPRO: IPR001548; Peptidase M2.
CC InterPro: IPR006025; Zn_Mtpeptidse.
CC Pfam: PF01401; Peptidase M2; 2.
CC PRINTS: PR00791; PEPTIDASEA.
CC PRODOM: PD004184; Peptidase M2; 2.
CC PROSITE: PS00142; ZINC_PROTEASE; 2.
CC Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;
KW Glycoprotein; Transmembrane; Repeat; Signal; Alternative splicing.
FT SIGNAL 1 35
FT CHAIN 36 1313
FT ISOFORM
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT
FT ZINC 1 (CATALYTIC) (BY SIMILARITY).
FT ZINC 1 (BY SIMILARITY).
FT ZINC 1 (CATALYTIC) (BY SIMILARITY).
FT ZINC 2 (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 396 397
FT METAL 396 397
FT ACT_SITE 397 397
FT METAL 400 400
FT METAL 994 994
FT ACT_SITE 994 995
FT ACT_SITE 995 995

FT METAL 998 998
FT CARBOHYD 44 44
FT CARBOHYD 60 60
FT CARBOHYD 80 80
FT CARBOHYD 117 117
FT CARBOHYD 152 152
FT CARBOHYD 166 166
FT CARBOHYD 224 224
FT CARBOHYD 515 515
FT CARBOHYD 683 683
FT CARBOHYD 701 701
FT CARBOHYD 720 720
FT CARBOHYD 766 766
FT CARBOHYD 948 948
FT CARBOHYD 1197 1197
FT VARIANT 207 207
SQ SEQUENCE 1313 AA; 150907 MW; 8C85D0015F129591 CRC64;

Query Match 30.5%; Score 1310; DB 1; Length 1313;
Best Local Similarity 42.0%; Pred. No. 4.8e-84;
Matches 251; Conservative 115; Mismatches 214; Indels 18; Gaps 7;

QY 20 TIEQAKTFLDKFHEADLFYQSSLASWNTNITEVQNMNAGDKWAFLEQSTL 79
DB 650 TDEAKNFVEYDRTAKVLWNEYAEANWHNTNITEGSKLLQKKEVSHLKYGTW 709
QY 80 AQMPLOEIQLTVKQLQALQONGSSVLSDEKSKRLNTILNTMTSTIYTGKVCNPDNPQ 139
DB 710 AKTFDVSFQNSTKRIIKIQQNVDRVLPPELNEYNQILDMETTSVANVCYTG-- 767
QY 140 ECLLEPGELNEIMANSLDYNERLWAWESRSEVQKLRPLYYEYVVLNENARAHNEDY 199
DB 768 TCSLEPDLTNIMATSRKYEBELLWYKSWRDKVGRALFFPFKYVDFSNKIAKLNGYSDA 827
QY 200 GDYMRGDYEVNGDGYDYRSQGLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP 258
DB 828 GDSWSSVSEDDLE-----QDLEKLYQELQVLYNLHAYVRRSLHRHGYSEYNL 877
QY 259 IGLFAHLGDMGWFNLSLTVPFQKQKNDIVTDAMVDQANDQRIKFAEKFFVSV 318
DB 878 DGPIFAHLGNWAGTWSNIYDLVAPFSPASIDATEAMIKQGTTPRIFKEADNFFTSL 937
QY 319 GLPNTQGFWNSMLTDGYNQKAVCHPTAMDGK-DFRILMCTKVMTDDFLTAHBMG 377
DB 938 GLLPVPFPFWKSMLEKTDGSEVVCASANDFYNGKDFRIKQCTSVNWEELVIAHBMG 997
QY 378 HIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSGLLSPDQEDNETIN 437
DB 998 HIQYPMQYKDLPTVTFEGANPGFHEAIGDVLALSYSTPKHLHLLSSE-GSGYEHDIN 1056
QY 438 FLLKQALITVGLTPETYMLEKRWNVFKEIPEKDCOMKMKWEMKREIVGVVPEVPHDET 497
DB 1057 FLMKWALDKIAFIPFYSYLDQWREVFQSTKENYQNSWLSRLKYQGLCPVPRSQGD 1116
QY 498 CDPASLFHVSNDYSFIRYRTLYQFCEALCOAAKHEGPHLHKCDISNSTAGOKLFNM 557
DB 1117 FDPGSKFHPANVPVIRYFISIIQFQFHEALCRAAGHTGPLYKCDIYQSKAAGLLADA 1176
QY 558 LELGKSEPTWALENVGAKNVAZPLNLYPELFTWLDKQNK--NSFVGM-STOWSP 612
DB 1177 MKLGYSQKQPEAMKIIITGPNMSASAINMYFAPLTWLTENRRHGETLIGWPEYTWTP 1234

RESULT 7
ACE_RABIT
ID ACE_RABIT STANDARD; PRT; 1310 AA.
AC P12822; 002852;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1)
DE (ACE) (Dipeptidyl carboxypeptidase I) (Kininase II).
GN ACE OR DCPI.

OS Oryctolagus cuniculus (Rabbit).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=92179960; PubMed=1311831;
RA Thekkumkara T.J., Livingston W. III, Kumar R.S., Sen G.C.;
RT "Use of alternative polyadenylation sites for tissue-specific
transcription of two angiotensin-converting enzyme mRNAs.";
RL Nucleic Acids Res. 20:683-687(1992).
RN [2]
RP REVISIONS.
RX KARUMKARA T.J., SEN G.C.;
RA "The mRNAs encoding the two angiotensin-converting isozymes are
transcribed from the same gene by a tissue-specific choice of
alternative transcription initiation sites.";
RL J. Biol. Chem. 266:3854-3862(1991).
RN [4]
RP SEQUENCE OF 34-55.
RC TISSUE=Lung;
RX MEDLINE=84051289; PubMed=6314908;
RA Iwata K., Blacher R., Soffer R.L., Lai C.Y.;
RT "Rabbit pulmonary angiotensin-converting enzyme: the NH2-terminal
fragment with enzymatic activity and its formation from the native
enzyme by NH4OH treatment.";
RL Arch. Biochem. Biophys. 227:188-201(1983).
CC -!- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF
THE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF THE
VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN.
CC -!- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,
oligopeptide-|-Xaa-Xbb, when Xaa is not Pro, and Xbb is neither
Asp nor Glu. Converts angiotensin I to angiotensin II.
CC -!- COFACTOR: Binds 2 zinc ions (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=Somatic;
IsoId=PI2822-1; Sequence=Displayed;
Name=Testis-specific;
IsoId=F22968-1; Sequence=External;
PIR, S35484; S35484.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
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or send an email to license@isb-sib.ch).
EMBL; X62551; CAA44428.1; --
DR EMBL; M58579; AAA31151.1; ALT_SEQ.
DR PIR, S35484; S35484.
DR MEROPS; M02.003; --
DR InterPro; IPR001548; Peptidase_M2.
DR InterPro; IPR006025; Zn_MTPeptide.
DR Pfam; PF01401; Peptidase_M2; 2.
DR PRINTS; PR00791; Peptidase_M2.
DR PRODOM; PD004184; Peptidase_M2; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; 2.
KW Hydrolase, Metalloprotease, Carboxypeptidase, Zinc, Dipeptidase;
FT Glycoprotein, Transmembrane, Repeat, Signal; Alternative splicing.
FT SIGNAL 1 33
FT CHAIN 34 1310 ANGIOTENSIN-CONVERTING ENZYME, SOMATIC

FT DOMAIN 34 1263
FT TRANSMEM 1264 1280
FT DOMAIN 1281 1310
FT REPEAT 232 588
FT REPEAT 829 1185
FT METAL 395 395
FT ACT_SITE 396 396
FT METAL 399 399
FT METAL 992 992
FT ACT_SITE 993 993
FT METAL 996 996
FT CARBOHYD 59 59
FT CARBOHYD 79 79
FT CARBOHYD 151 151
FT CARBOHYD 323 323
FT CARBOHYD 449 449
FT CARBOHYD 513 513
FT CARBOHYD 681 681
FT CARBOHYD 699 699
FT CARBOHYD 718 718
FT CARBOHYD 946 946
FT CARBOHYD 1195 1195
FT CONFLICT 48 48
SQ SEQUENCE 1310 AA; 150405 MW; 04777FAB17981DEA CRC64;

Query Match 29.9%; Score 1283.5; DB 1; Length 1310;
Best Local Similarity 36.8%; Pred. No. 3.5e-82;
Matches 275; Conservative 135; Mismatches 262; Indels 75; Gaps 17;

Qy 7 LLSLVAVTAAGSTI-----EQAKTFDKFNHEADLFYQSSLASWYNTNI 54
Db 21 LLLLLRPPPAALTLDPLGDFADAEAGALFASSYNSABQVLFRTSTAASWAHDTNI 80

Qy 55 TEENVQNMNAGDKWSAFLEKEOSTLAQMYPOE1-----QNLTV--VKLQALQONGSS 106
Db 81 TANARQEB-----EALLSQFAEAWGKAKELDYPWQNTDPELRILIGAVRTLGA 135

Qy 107 VLSEDKSKRLNTILNTMTSTIYTGKVCNPDNPQECLELLPEGLNEIMANSLDNERLWANE 166
Db 136 NLPLAKRQQVNSLLSNMSQIYSTGKVCPPNKATSCWSLDPDLNLIASSRSYAMLLFAWE 195

Qy 167 SWSEVKGQIRPLYEEVVLKEMARAHVEDYDWRGDYEVNGVDYDSRGQIIEVD 226
Db 196 GWNNAVGIPLKPLYQEFALSNAYQDGFSDTGAYRWSYDSTPE-----EDL 245

Qy 227 EHTPEEIKPLYEHLHAYVRRAKLMNAY-PSYISPGICLPAHLGDMWGRFWTNLYSTVDF 285
Db 246 ERIYHQLEPLYLNHAYVRRVLRHRYGDRYINLRGPIPAHLGDMWMAQSWESIYDMVVPF 305

Qy 286 GQKPNIDVTDAVDQAWDAQRIEKEAKFPVSGLPNMTGQFWNSMLTDPGVQKAVCH 345
Db 306 PDKPNLDVTSTWYQKGNATHMPRVAEEFTSLGLLPMPPEFWAESMLEKPEDEGVVCH 365

Qy 346 PTAWDL-GKGDFTILMCTKVTMDDFLTAHEMIGHIYDMAYAAQPFLLRNGANEGTHEAV 404
Db 366 ASAWDFYNRKDFRIKQCTQVTMTDQLSTVHEMGMHVQYLYQYKQDPVSLRR-ANPGFHEAI 424

Qy 405 GEINSLSAATPKLXSLGILLSPQEDNETEINFLIKQALTIVGLTPTVLMLEKRWVWF 464
Db 425 GDVLALSVSPTFAHLKTKGLLD-HVTNDESDINYLKNALEKTAFLPFGVLVDQWGVF 483

Qy 465 KGEIPKQWKKWEMEREIVGVVEVPVPHDETCDPASLPHVSNDSYFIRYTRTYQFQ 524
Db 484 SGRTFSSRYNFDWYLLATKYCGICPPVVRNETHFDAGAKPHIPSVTPYIRYFVSVLQFQ 543

Qy 525 PQEALCOAAKHGELHKCDI-SNSTEAGQKLFNMLRLGKSEPTWALLENVVGAKMNVRL 584
Db 544 FHOALCMAGHQGLHQCIDIYQSTRAGAKLRAVLQAGCSRPOEVLKQMWVASDALDAQPL 603

Qy 595 LNYPELFTMLKQONKNS--FVGM-STDWSPYADQSIKVRISLSKSLG-----DKA 632
Db 604 LDYFPQVTQWLQEQNERNGEVLGHPEYQWEPPLPNNYPEGIDLVTDAAEASRFVEEYDRS 663

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QY 633 YE-WND-----NEMYLFRSVAYAMQVFLKVNQMLFGEDVVRVANLKPRIENF 684
DB 664 FQAVNVEAYEANYNTTITASKILLQKMOIANHTLYG-----NNAARFVDSNF 716
QY 685 VTAP-----KNVSD-----IIPRTVEK 702
DB 717 QNATSKRIIKVQLQRAVLVPELES 743

RESULT 8
ACET RABBIT
ID ACET RABBIT STANDARD; PRT; 737 AA.
AC P22968;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Angiotensin-converting enzyme, testis-specific isoform precursor
DE (EC 3.4.15.1) (ACE-T) (Dipeptidyl carboxypeptidase I) (Kininase II).
OS ACE OR DCPI.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white; TISSUE=Testis;
RX MEDLINE=89380303; PubMed=2550457;
RA Kumar R.S., Kusari J., Roy S.N., Soffer R.L., Sen G.C.;
RT "Structure of testicular angiotensin-converting enzyme. A segmental
RT mosaic isoform."
RL J. Biol. Chem. 264:16754-16758(1989).
RN [2]
RP SEQUENCE OF 1-117 FROM N.A.
RX MEDLINE=91139683; PubMed=1847388;
RA Kumar R.S., Thekkumkara T.J., Sen G.C.;
RT "The mRNAs encoding the two angiotensin-converting isozymes are
RT transcribed from the same gene by a tissue-specific choice of
RT alternative transcription initiation sites."
RL J. Biol. Chem. 266:3854-3862(1991).
CC -!- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF
CC THE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF THE
CC VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN.
CC -!- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,
CC oligopeptide.-Xaa-Xbb, when Xaa is not Pro, and Xbb is neither
CC Asp nor Glu. Converts angiotensin I to angiotensin II.
CC -!- COFACTOR: Binds 1 zinc ion (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Testis-specific;
CC IsoId=P22968-1; Sequence=Displayed;
CC Name=Somatic;
CC IsoId=P12822-1; Sequence=External;
CC -!- TISSUE SPECIFICITY: SPERMATOCTYES, ADULT TESTIS.
CC -!- INDUCTION: EXPRESSION IS THOUGHT TO BE SUBJECT TO HORMONAL
CC REGULATION BY ANDROGENS.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
CC
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CC
CC -----
CC EMBL; J05041; AAA31153.1; -
CC EMBL; M58580; AAA31152.1; -
CC PIR; A34402; A34402.
CC MEROPS; M02.004; -
CC InterPro; IPR001548; Peptidase M2.
CC InterPro; IPR006025; Zn_MTPeptide.
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DR Pfam; PF01401; Peptidase M2; 1.
DR PRINTS; PRO0791; PEPTIDASEA.
DR PRODOM; PDC04184; Peptidase M2; 1.
DR PROSITE; PS00142; ZINC PROTEASE; 1.
KW Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;
KW Glycoprotein; Transmembrane; Testis; Signal; Alternative splicing.
FT SIGNAL 1 32
FT CHAIN 33 737
FT DOMAIN 33 690
FT TRANSMEM 691 707
FT DOMAIN 708 737
FT METAL 419 419
FT ACT SITE 420 420
FT METAL 423 423
FT METAL 447 447
FT DISULFID 188 194
FT DISULFID 388 406
FT DISULFID 574 586
FT CARBOHYD 108 108
FT CARBOHYD 126 126
FT CARBOHYD 145 145
FT CARBOHYD 373 373
FT CARBOHYD 622 622
FT SEQUENCE 737 AA; 83923 MW; FC43CCT76655C3DCA CRC64;
Query Match 29.9%; Score 1283; DB 1; Length 737;
Best Local Similarity 40.8%; Pred. No. 1.7e-82;
Matches 250; Conservative 112; Mismatches 213; Indels 38; Gaps 10;
QY 20 TIEQAQATFDKFNHEAEDLFYQSSLASNNYNTNITEB-----NVQNMN--AGDKW 69
DB 75 TDEASRFRVEEDRSFQAVNWEYAEANNYNNTNITEASKILLQKMOIANHTLYGNW 134
QY 70 SAFLKEOSTLAQMYPLQEIQLNFKVLOALQONGSVLSSEKSKRLNTILNTMTTIST 129
DB 135 -----ARRFDVSNFQATSKRIKKVQDQRAVLVPELKEBEYNOILLDMETIYSV 184
QY 130 GKVCNPDNPECLLPEGLNEIMANSLDYNERLWAMESWRSEVGKOLRLPYEYVVKNE 189
DB 185 ANVCRVDG--SCQLPEFLTNLMTSKYDELLWWTNRDKVGRALVPPFYKVEFINK 242
QY 190 MARANHYEDYGVWGDYEVNGVDYSGRGQLIEDVHTFBEIKPLYEHLHYVRAKLM 249
DB 243 AARLNGVVDAGDSWRSMYETPTLE-----QDLERLFOELQPLYNLHAYYGRALH 292
QY 250 NAY-PSYISIGCLPAHLGDMWGRFTNLYSLTVFGQKPNIDVTDAVDAQDAQRIF 308
DB 293 RHYGAQHINLEGPAPALLGNWMAQIWSNIYDLVAPFPASATMDATEAMIKGWTPRWF 352
QY 309 KEAKFPVSVGLPNMTQGFWENSLTDPGNVQKAVCHPTAWDLKG-DPRILMCTKVIMD 367
DB 353 EADKFFISLGLLFPVPPPEFWNKSLEKPTDGEVWCHASAWDFYKQDPRIKQCTTVNNE 412
QY 368 DFLTAHEMGHIOYDMAYAAQPTLLRNGANEGPHEAVGIMSLSAATPKHLSIGLLSPD 427
DB 413 DLVVVHEMGHIQYFMOYKDLPLVALREGANPGPHEAIGDVALSVSTPKELHSINLSSE 472
QY 428 PQENETETNPLKQALITVGTLPFTYMLEKRWNVFKGEIPKQDKQWKKWKEBIVGV 487
DB 473 -GGGYEHINFLMKMALDKIAFPFSYLVDEWRWRVFDGSIITKENYNQEWWSLRKYQGL 531
QY 488 VEPVPHETVCDPASLFHVSNDYSFIRYTRTYLQFQFOEALCOAAKHEGPHLKCDISNS 547
DB 532 CPPAPRSQGDFFGAKFHISSVPIRYRVSVFTIQFQHEALCKAAGHTGPLHTCDIYQS 591
QY 548 TEAQCKLFNMLRLOKSEPTWLTALENVVGAKNMVRPLLYFPLFTWLKQDN--KNSFVG 605
DB 592 KEAGKRLADAMKLGYSKPWPEAMKVITGQPNNSASAMNYPKPLMDWLLTENGHGEKUG 651
QY 606 W-STDWSPYADQS 617
DB 652 WPOYTWTPNSARS 664
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RESULT 9
 ACE_DROME STANDARD; PRT; 615 AA.
 ID Q10714; Q27572; Q9NKE4; Q9TX66; Q9JVJ3;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Angiotensin-converting enzyme precursor (EC 3.4.15.1) (Dipeptidyl
 DE carboxypeptidase 1) (Kininase II).
 GN ANCE OR RACE OR BG:DS08220.3 OR CG8827.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=94040210; PubMed=8224398;
 RA Corneli M.J., Coates D., Isaac R.E.;
 RT "Characterisation of putative Drosophila angiotensin converting enzyme
 RT cDNA clones";
 RL Biochem. Soc. Trans. 21:243-243(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=95293950; PubMed=7775412;
 RX Corneli M.J., Williams T.A., Lamango N.S., Coates D., Corvol P.,
 RA Soubrier F., Hohelsel J., Lehrach H., Isaac R.E.;
 RT "Cloning and expression of an evolutionary conserved single-domain
 RT angiotensin converting enzyme from Drosophila melanogaster";
 RL J. Biol. Chem. 270:13613-13619(1995).
 RN [3]
 RP REVISIONS.
 RA Corneli M.J.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S;
 RX MEDLINE=96028519; PubMed=7547464;
 RA Tatei K., Cai H., Ip Y.T., Levine M.;
 RT "Race: a Drosophila homologue of the angiotensin converting enzyme";
 RL Mech. Dev. 51:157-168(1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=99403001; PubMed=10471707;
 RA Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R.G., Davis T.,
 RA Doyle C., Galle R.F., George R.A., Harris N.L., Hartzell G.,
 RA Harvey D., Hong L., Houston K.A., Hoskins R.A., Johnson G.,
 RA Martin C.H., Moshrefi A., Palazzolo M., Reese M.G., Spradling A.C.,
 RA Tsang G., Wan K.H., Whitelaw K., Celnikier S.E., Rubin G.M.;
 RT "An exploration of the sequence of a 2.9-Mb region of the genome of
 RT Drosophila melanogaster: The Adh region";
 RL Genetics 153:179-219(1999).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Arif J.J., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brotter P.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Daw I., Dietz S.M.,

Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy L., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely; TISSUE=Embryo;
 RX MEDLINE=22426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Guan H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celnikier S.E.;
 RT "A Drosophila full-length cDNA resource";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 CC -!- FUNCTION: MAY PLAY A ROLE IN THE CONTRACTIONS OF THE HEART, GUT
 CC AND TESTES.
 CC -!- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,
 CC oligopeptide.-Xaa-Xbb, when Xaa is not Pro, and Xbb is neither
 CC Asp nor Glu. Converts angiotensin I to angiotensin II.
 CC -!- COFACTOR: Binds 1 zinc ion (by similarity).
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE AMNIOBLASTS DURING GERM BAND
 CC ELONGATION, SHORTENING AND HEART MORPHOGENESIS. EXPRESSED IN
 CC MIDGUT THROUGHOUT EMBRYOGENESIS.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
 CC -----
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 CC -----
 CC EMBL; U25344; AAB02171.1; -;
 CC EMBL; U34599; AAC46902.1; -;
 CC EMBL; A2003408; AAF44834.1; -;
 CC EMBL; A2003641; AAF53353.2; -;
 CC EMBL; AY061129; AAL28677.1; -;
 CC MEROPS; W02.003; -;
 CC FlyBase; FBgn0012037; Ance.
 CC GO; GO:0004246; F:peptidyl-dipeptidase A activity; IDA.
 CC InterPro; IPR001548; Peptidase M2.
 CC InterPro; IPR006025; Zn_Mtpeptidse.
 CC Pfam; PF01401; Peptidase M2; 1.
 CC PRINTS; PR00791; PEPTIDASEA.
 CC ProDom; PD004184; Peptidase M2; 1.
 CC PROSITE; PS00142; ZINC_PROTEASE; 1.
 CC HydroLase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;
 CC Glycoprotein; Signal.
 CC SIGNAL 18 615 POTENTIAL.
 CC CHAIN 1 17 ANGIOTENSIN-CONVERTING ENZYME.
 CC METAL 367 367 ZINC (CATALYTIC) (BY SIMILARITY).

FT ACT SITE 368 368 BY SIMILARITY.
 FT METAL 371 371 ZINC (CATALYTIC) (BY SIMILARITY).
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 311 311 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 48 51 WAYG -> GPMR (IN REF. 4).
 FT CONFLICT 141 141 C -> S (IN REF. 4).
 FT CONFLICT 293 293 G -> A (IN REF. 3).
 FT CONFLICT 346 346 I -> T (IN REF. 5, 6 AND 7).
 FT CONFLICT 365 365 V -> E (IN REF. 1).
 FT CONFLICT 402 402 S -> A (IN REF. 1).
 FT CONFLICT 414 414 I -> T (IN REF. 1).
 FT CONFLICT 486 486 S -> T (IN REF. 4).
 FT CONFLICT 533 533 V -> M (IN REF. 4).
 FT CONFLICT 547 547 A -> R (IN REF. 3).
 SQ SEQUENCE 615 AA; 70926 MW; 983F9A41C5B9485 CRC64;

Query Match 25.3%; Score 1085; DB 1; Length 615;
 Best Local Similarity 36.4%; Pred. No. 1.1e-68;
 Matches 223; Conservative 122; Mismatches 245; Indels 22; Gaps 9;

QY 8 LLSLVAVTAQAOSTIERQAKTFLDKFNHEAEDLFYQSSLASMNNTNTEENVQNNAGD 67
 DB 8 LLAVLAVTQALVKEIQAEVLEMLNKLAKRTNVTETAAWAGSMITTENKKNEISA 67
 QY 68 KWSAFLEKQSTLAQMYPLQEIQLNLTVKLQALQNGSSVLSDEKSKRLNTILNTMSTIY 127
 DB 68 ELAKFMKEVASDITTKFQWRSYQSDLRQPKALTKLGYAAPDDYAEALLDTLSAMESNF 127
 QY 128 STGKVCNPNPOEC-LLLEPGLNEIMANSLDYNERLWAWESRSEVGKOLRPLRYEYVVL 186
 DB 128 AKVKVCKYKSTKCDLADPEIEVSKSRDHELAYWREFYDKAGTAVRSOFERYVEL 187
 QY 187 KNEWANANHYEDYGDYWRGVDYVNGVDYSGRQLIEDVEHTFEIKPLYEHLHAYRA 246
 DB 188 NTKAALNNFTSGAEAWLDEYE-----DQTEFOQLEDI---FADIRPLYQOIHGYRF 237
 QY 247 KLMWAY-PSYISPIGCLPAHLGLGDMGCFWNTNLYSLTVPGQKPDNDVTDAVMVDQAWDAQ 305
 DB 238 RLKHYGDVAVSEGTGPIPMHLLGNWQAQNSEADIVSPPEKPLVDVSAEKEKQYTP 297
 QY 306 RIFKEAKFVSVGLPNNVQGFENSMMLTDPGNVQKAVCHPTAWDLGK-GDFRILMCTKV 364
 DB 298 XMFQMGDDFFTSNNLTKLPQDFWDKSIIEKPTGRDLVCHASAWDFYLLDDVRIKQCTRV 357
 QY 365 TMDDFLTAHEMGIHQYDMAVAAQPFLLRNGAEGHEAAGEVETMSLSAATPKHLKSIQL 424
 DB 358 TDQQLFTVHELHGHQYFLOVQHPFYRTGAPFGHEAGVGLSVSTPKLEKIGLL 417
 QY 425 SPDOENETEINFLKQALTVITGLPTFMLEKRWMPVFKGIPKDDQWKKWENKREI 484
 DB 418 K-DYVRDDEARINQLFUTALDKIVFLPFAFTMDKYRSLFRGSDVXANNWCAFWKLIRDEY 476
 QY 485 VGVPEVPHDTCYDPAFLFHSNDYSFIRYRTLYQFOFQALC-QAAKH-----EOP 538
 DB 477 SGIEPPVVRSEKDFDAKTHISADVEYLYLVFIQYQYKSAICAKAGQDPNVLP 536
 QY 539 LHKDCINSTEAGOKLFNMLGKSEPTWLTALENVGAKNVRPLNLTPEPLFTWLKQDQ 598
 DB 537 LDNCDIYGSAAAGAAFNMLSMGAKPWPDALEAFNGERIMSGKATAEYFEPLRVNLEAE 596
 QY 599 N--KNSFVGWST 608
 DB 597 NIKNVHIGWTT 608

RESULT 10
 ACE HAEIE
 ID -ACE HAEIE
 AC Q10715;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Angiotensin-converting enzyme precursor (EC 3.4.15.1) (Dipeptidyl
 DE carboxypeptidase I) (Kinase II).
 GN ACE.
 OS Haematobia irritans exigua (Buffalo fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea;
 OC Muscidae; Haematobia.
 OK NCBI_TaxID=34678;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96215437; Pubmed=8647080;
 RA Wijffels G.L., Fitzgerald C., Gough J., Ridding G.A., Elvin C.,
 RA Kemp D.J., Willadsen P.,
 RT "Cloning and characterisation of angiotensin-converting enzyme from
 RT the dipteran species, Haematobia irritans exigua, and its expression
 RT in the maturing male reproductive system.";
 RL Eur. J. Biochem. 237:414-423(1996).
 CC -!- FUNCTION: INVOLVED IN THE SPECIFIC MATURATION OR DEGRADATION OF A
 CC NUMBER OF BIOACTIVE PEPTIDES.
 CC -!- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide.
 CC oligopeptide-|-Xaa-Xbb, when Xaa is not Pro, and Xbb is neither
 CC Asp nor Glu. Converts angiotensin I to angiotensin II.
 CC -!- COFACTOR: Binds 1 zinc ion (By similarity).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE COMPOUND GANGLION AND IN THE
 CC POSTERIOR REGION OF THE MIDGUT.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L43965; AAA70427.1; -;
 DR PIR; S65472; S65472.
 DR MEROPS: M02.003; -;
 DR InterPro; IPR001548; Peptidase M2.
 DR InterPro; IPR006025; Zn_MTPeptidase.
 DR Pfam; PF01401; Peptidase M2; 1.
 DR PRINTS; PR00791; PEPDPTASEA.
 DR PRODOM; PD004184; Peptidase M2; 1.
 DR PROSITE; PS00142; ZINC PROTEASE; 1.
 KW Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;
 KW Glycoprotein; signal.
 FT SIGNAL 1 17 POTENTIAL
 FT CHAIN 18 611 ANGIOTENSIN-CONVERTING ENZYME
 FT METAL 367 367 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT SITE 368 368 BY SIMILARITY.
 FT METAL 371 371 ZINC (CATALYTIC) (BY SIMILARITY).
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 531 531 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 611 AA; 70505 MW; A43D6DFA83ECB53 CRC64;

Query Match 24.7%; Score 1058; DB 1; Length 611;
 Best Local Similarity 37.3%; Pred. No. 8.7e-67;
 Matches 223; Conservative 108; Mismatches 246; Indels 22; Gaps 7;

QY 8 LLSLVAVTAQAOSTIERQAKTFLDKFNHEAEDLFYQSSLASMNNTNTEENVQNNAGD 67
 DB 8 ILAGLVCHGATKEIVATEYLQNINKELAKHTNTEVTSWAYASNTIDENERLNEISA 67
 QY 68 KWSAFLEKQSTLAQMYPLQEIQLNLTVKLQALQNGSSVLSDEKSKRLNTILNTMSTIY 127
 DB 68 ENAKFLKEVAKDITQKFNWRTYGSADVRRQFKSLSTGYSALEPAEDYAEELVLSAMESNF 127
 QY 128 STGKVCNPNPOEC-LLLEPGLNEIMANSLDYNERLWAWESRSEVGKOLRPLRYEYVVL 186
 DB 128 AKVRVCDYKNSAKCDLSLQPEIEIITKSRDPEELKYVWTQFYDKAGTPTRSNPEKYVEL 187
 QY 187 KNEWANANHYEDYGDYWRGVDYVNGVDYSGRQLIED-VEHTFEIKPLYEHLHAYR 245

Db	188	NTKSALNNFTGAEVWLDVEY-----DATFEDQLEALFEDIKELYDQVHGYYR	236
Qy	246	AKLNNAY-PSYISPIGCLPAHLLGDWGRFWNNLYSLTFPGQKPNIDVTDAMVDQAMD	304
Db	237	YRLNKEYIGDEVVSKTGPLPMHLLGNMAQQSSSIADIVSPPEKPLVDVSDENVAQGYTP	296
Qy	305	QRITFEKAERFFVSVGLPNNNTQGFWNSMLTDPGNVQKAVCHPTADWLG-KGDFRILMCTK	363
Db	297	LKMFQMGDDPFFQSMGLKKLPQEFNDKSLILKPDGGRDLVCHASANDFYLTDVRIKQCTR	356
Qy	364	VTWDDFLTAHHNGHIOYDMAVAAQFFLLRNGANEGHEAVGEIMSIASAATPKHLKSI	423
Db	357	VTQDQFFTVHHMGHIOYFLQHQHFFVYRTGANGPGEHFAVGDVLSVSTPKHLRERVL	416
Qy	424	LSPDFQEDNETEIFLLKQALITVGLTFYTMLEKRWMMVFKGIPKQDMMKXWMSKRE	483
Db	417	LK-NYVSDNEARINQLFTALDKIVLFPFAFTMDKYRWALFRGOADKSEWNCAPWKLREE	475
Qy	484	IUGVVEPVPHDETYCDPASLFVSNDSYGFIRYRTTLVQFOFQBALCOAA-----KHG	537
Db	476	YSGIEPPVYRTKDFADPAKHVSDVLYRLVSLFIQFYKSACTITAGEVVPNQTEY	535
Qy	538	PLHKCDISNSTBAGQKLFNMLRLGKSEPWTLALENVVCAKMMVRPLNLYFEPLFTWLK	596
Db	536	PLDNCDIYKSGAGKLFENKLSLGASKWPDPALFAFNERTMTGKAIAEYFEPLRWLSE	594
RESULT 11			
YFWA_BACSU			
ID	YFWA_BACSU	STANDARD;	PRT; 501 AA.
AC	P50848;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DE	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Hypotheoretical metalloprotease yfwA (EC 3.4.24.-).		
GN	yfwA.		
OS	Bacillus subtilis.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1423;		
ON	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=168 / Marburg;		
RY	MEDLINE=96349105; PubMed=8760912;		
RA	Sorokin A.V., Azevedo V., Zumschein E., Galleron N., Ehrlich S.D.,		
RA	Serror P.;		
RT	"Sequence analysis of the Bacillus subtilis chromosome region between		
RT	the serA and kds loci cloned in a yeast artificial chromosome.",		
RL	Microbiology 142:2005-2016(1996).		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=168;		
RY	MEDLINE=98044033; PubMed=9384377;		
RA	Kunst F., Ogawara N., Moszer I., Albertini A.M., Alloni G.,		
RA	Azevedo V., Bessieres P., Bolotin A., Borchert S.,		
RA	Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,		
RA	Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,		
RA	Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,		
RA	Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,		
RA	Ertan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,		
RA	Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,		
RA	Ghim S.Y., Glaeser P., Goffeau A., Gollightly E.J., Grandi G.,		
RA	Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,		
RA	Harbert B., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,		
RA	Joris B., Karanata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,		
RA	Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,		
RA	Kurita K., Lapidus A., Lardiniois S., Lauber J., Lazarevic V.,		
RA	Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,		
RA	Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,		
RA	Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudenga B., Park S.H.,		
RA	Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,		
RA	Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,		
RA	Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie		

Db 451 HPIK-----QWTEKHVHGKRRKPLDKIDATG-BELNRYLIDY 490

RESULT 12

GLGB BACSU

ID P39118; STANDARD; PRT; 627 AA.

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching enzyme).

DE enzyme).

GN GLGB.

OS Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1423;

RN [1] SEQUENCE FROM N.A.

RP STRAIN=168;

RC MEDLINE=94195107; PubMed=8145641;

RX Kiel J.A.K.W., Boels J.M., Beidman G., Venema G.;

RA "Glycogen in Bacillus subtilis: molecular characterization of an operon encoding enzymes involved in glycogen biosynthesis and degradation."

RT Mol. Microbiol. 11:203-218(1994).

RL [2] SEQUENCE FROM N.A.

RP STRAIN=168;

RC MEDLINE=98048467; PubMed=9387221;

RX Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;

RA "Sequencing and functional annotation of the Bacillus subtilis genes in the 200 kb rnb-dnaB region."

RT Microbiology 143:3431-3441(1997).

RL [3] SEQUENCE FROM N.A.

RP STRAIN=168;

RC MEDLINE=98044033; PubMed=9384377;

RX Kunat F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Bortiss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz S., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Medina N., Meliado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Pressecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takanashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandendol M., Vannier P., Vassarotti A., Viari A., Wambutt R., Wedler H., Wedler H., Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;

RT "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis".

RL Nature 390:249-256(1997).

CC -!- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic linkages in glycogen by scission of a 1,4-alpha-linked oligosaccharide from growing alpha-1,4-glucan chains and the subsequent transfer of the oligosaccharide to other parts of

CC alpha-1,4-glucan chains.

CC -!- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of glycogen.

CC -!- PATHWAY: Glycogen biosynthesis; third step.

CC -!- INDUCTION: EXPRESSED EXCLUSIVELY ON MEDIA CONTAINING CARBON SOURCES THAT ALLOW EFFICIENT SPOULATION.

CC -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.

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CC -----

DR EMBL; Z25795; CAA81040.1; --

DR EMBL; AF008220; AAC00214.1; --

DR EMBL; Z99119; CAB15076.1; --

DR PIR; S4C048; S40048.

DR Subtilist; BG10907; glgB.

DR InterPro; IPR006047; Alpha_amyl_cat.

DR InterPro; IPR006407; GlgB.

DR InterPro; IPR004193; Glyco_hydro_13N.

DR Pfam; PF00128; alpha-amylase; 1.

DR Pfam; PF02922; isoamylase N; 1.

DR TIGRFAMs; TIGR01515; branching_enzym; 1.

KW Glycogen biosynthesis; transferase; Glycosyltransferase;

KW Complete proteome.

FT ACT_SITE 309 309 BY SIMILARITY.

FT ACT_SITE 352 352 BY SIMILARITY.

FT ACT_SITE 420 420 BY SIMILARITY.

SQ SEQUENCE 627 AA; 73665 MW; 64B0A553B67BA CRC64;

Query Match 2.9%; Score 125; DB 1; Length 627;

Best Local Similarity 18.6%; Pred. No. 0.41;

Matches 131; Conservative 86; Mismatches 225; Indels 264; Gaps 37;

QY 49 NYNTNTEENVQNNMAGDKWSAFI-----KEOSTLAQWYFLOEIQNLTVKQLQALQON 103

DB 56 DFNWSGGEHVRHVRNDNGIWTLPFGIGEKER-----YKYEIVTN-----N 97

QY 104 GSSVLSEDKSKRLNLTNTWTSTYTGKVCNPNPQECLELLEPGLMEIMAN--SLDYNER 161

DB 98 GEIRLKADP-----YAIYS-----EVRENTASLTIDLE 125

QY 162 LWAMESRSEYKQLRPLYEYVVLKNEMARANHEDYGDYWRGDEYVANGVDGYDSRQ 221

DB 126 GYSWQDQKWKQKAKTLYEKVFI-----YELHLGSMK-----KHSDGRHYSYKE 171

QY 222 LIEOV-----EETFE--EIKPLYEHLHAYVRKLMNAYPSYISPIGCLPAHLGDMWGRF 274

DB 172 LSQTLIPYIKKHGTHIELLPVYB--HPYDRS-----WGQY 205

QY 275 WTNLYSLTVPFQKPNIDVTDAWVQA-----WDAQRIFKEABKFFVSVGLPNMT 324

DB 206 GTGYSPTSRFG--PPHDLN-KFVDECHQONIGVILDWVPGHFCKOAHGLYMFDEGEP--- 259

QY 325 QGFVNSMLTDPGNVQKAVCHPTAWDJKGDFRLMCTKVTMDDELTAH----HEMGHIQ 380

DB 260 --LVEYKEERDEN-----WLGATNFDI-----GKPEVHSFLISNLYAEFYHL- 303

QY 381 YDMAYAAQPLLRNANGNEGPH-EAVGIMSLSAATPKHLSIGLLSPDFQEDNETEINFL 439

DB 304 -----DGFVDAVANILYMPNQDERH-----TNPYAVDFL 333

QY 440 LKQALTIIVGLTLPFTYML--EKWRWVWFKGIPIKD-----QWKKWEMKRETVVVEPV 491

DB 334 KKLNTMEAPHYWMAAEDSTEWPQTVGAVEGGLGFHYKNNWGW---MNDVLKWTETP 390

QY 492 PHDETCDPASLFFVNSNDYSFYRTYTYLTYQFOQEAALCOAAKHEGLHKHCKDISNTEAG 551

391	PEERHC-----HQLISFLL-----YAFSEHFVLPFSHDEVY-----G	425
552	QXLFNMJRLGKSPWTLALENVGAKNMVRPLNT-----FELFTWLK	596
426	KK--SLNKNPGDY-----QKPAQYRLLLGTYMHPKOKLIFGSEFAQDEW-K	473
597	DQNKNSFVGXSTDMSPYDOSI-----KVRISLSALGDKAYEWND--NEWYL	642
474	DTEQ---LDWFLDSFPMHQKSVFTODLRFYQKSLIYEHDRHQSEWIDVHNDEQSI	530
643	FRSSVAYAMQYELKVKNMILFGEEDYRVANLKPRISENFVFTAP	688
531	F-SPIRYQGH-----GEALVINCFTPVVYHQYGVGP	563

RESULT 13

EPID_STAEPP
 ID_EPIB_STAEPP STANDARD; PRT; 986 AA.
 AC P30135;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Epidermin biosynthesis protein epIB.
 DE EpIB.
 GN GN
 OS Staphylococcus epidermidis.
 CC Plasmid pTc 32.
 BA Bacteria; Firmicutes; Bacillales; Staphylococcus.

NCBI_TaxID=1282;
[1]
SEQUENCE FROM N.A.
STRAIN-TU 3298 / DSM 3095;
MEDLINE=2135237; PubMed=1740156;
Schnell N., Engelke G., Augustin J., Rosenstein R., Ungermann V.,
Goetz F., Eutian K.-D.;
"Analysis of genes involved in the biosynthesis of lantibiotic
epidermin.";
Eur. J. Biochem. 204:57-68(1992).
-!- FUNCTION: INVOLVED IN THE POSTTRANSLATIONAL MODIFICATION OF THE
LANTIBIOTIC EPIDERMIS.
-!- SUBCELLULAR LOCATION: POSSIBLY ASSOCIATED WITH, AND ANCHORED TO,
THE CYTOSOLIC SIDE OF THE MEMBRANE.
-!- SIMILARITY: TO B.SUBTILIS SPAB AND L.LACTIS NISB.

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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

```

RESULT 14
EGAL_BACME          STANDARD;          FRT; 1034 AA.
ID   EGAL_BACME
AC   C52847;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Beta-Galactosidase (EC 3.2.1.23) (Lactase).
GN   BGAM.
OS   Bacillus megaterium.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_taxID=1404;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DSM 319;
RA   Strey J.;
RL   Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC   -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-
CC       galactose residues in beta-D-galactosides.
CC   -!- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration

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Search completed: February 19, 2004, 19:50:14
Job time : 21 secs

XX 29-SEP-1999; 99WO-US22976.
 XX 30-SEP-1999; 98US-0163648.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Acton LS, Robison KE, Hsieh FY;
 XX WPI; 2000-293140/25.
 XX N-PSDB; AA12764.
 XX
 XX Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
 XX polypeptide useful for detecting an ACE-2 therapeutic for treating
 XX hypertension, congestive heart failure, myocardial infarction,
 XX atherosclerosis and renal failure.
 XX
 XX Claim 2; Fig 1; 138pp; English.
 XX
 XX The present sequence represents a human angiotensin converting enzyme-2
 XX (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
 XX sequence of the full length ACE-2 cDNA was determined from a clone
 XX obtained from a cDNA library prepared from mRNA of a human heart of
 XX a subject who had congestive heart failure. ACE-2 has significant
 XX sequence homologies with ACE enzymes, and has also been shown to
 XX hydrolyse angiotensin I into Aug. (1-9). The ACE-2 therapeutics are
 XX used to treat blood pressure related diseases and conditions, such as
 XX hypertension, congestive heart failure, chronic heart failure, acute
 XX heart failure, myocardial infarction, atherosclerosis and renal
 XX failure.
 XX
 XX Sequence 805 AA;
 XX
 XX Query Match 100.0%; Score 4291; DB 21; Length 805;
 XX Best Local Similarity 100.0%; Pred. No. 0;
 XX Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
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 DB 1 MSSSSWLLSLVAVTAQSTIEEQAKTFLDKFNHEADLFYQSSLASWNTNITEENVQ 60
 QY 61 MNMAGDKWAFLEKQSTLAQMYPLQEIQLNLTQVLQALQNGSVLSSEKSLANTIL 120
 DB 61 MNMAGDKWAFLEKQSTLAQMYPLQEIQLNLTQVLQALQNGSVLSSEKSLANTIL 120
 QY 121 NTWSTIYTGKVCNPNQPCLELLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180
 DB 121 NTWSTIYTGKVCNPNQPCLELLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180
 QY 181 EYVVLKNEAMARHVEDYGDYWRGDEYVNGVDYSGQLIEDVHTFEIKPLYEHL 240
 DB 181 EYVVLKNEAMARHVEDYGDYWRGDEYVNGVDYSGQLIEDVHTFEIKPLYEHL 240
 QY 241 HAYVRKLMNAYSISPIGCLPAHLLGDMGWFNTLSLVTPFGQKPNIDVTDAMVDQ 300
 DB 241 HAYVRKLMNAYSISPIGCLPAHLLGDMGWFNTLSLVTPFGQKPNIDVTDAMVDQ 300
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 DB 301 AWDQRIFKEAEKFFSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRLM 360
 QY 361 CTKVTMDDELTAHHEMGIQYDNAYAAQPELLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
 DB 361 CTKVTMDDELTAHHEMGIQYDNAYAAQPELLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
 QY 421 IGLLSPDFQEDNETEINFLLKQALITVGTLPFTYMLEKRWVMVFKEIPKQOMKKWEM 480
 DB 421 IGLLSPDFQEDNETEINFLLKQALITVGTLPFTYMLEKRWVMVFKEIPKQOMKKWEM 480
 QY 481 KREIVGVVPEVPHDETCDPASLPHVSNDSYFRYTRITLYQFOFQALCOAAKHEGPLH 540
 DB 481 KREIVGVVPEVPHDETCDPASLPHVSNDSYFRYTRITLYQFOFQALCOAAKHEGPLH 540

QY 541 KCDISNSTEAGQKLFNMLRLGKSEPTWLTALENVVGAANNVRLPILNFFPLFTWLKDQNK 600
 DB 541 KCDISNSTEAGQKLFNMLRLGKSEPTWLTALENVVGAANNVRLPILNFFPLFTWLKDQNK 600
 QY 601 NSFVGWSTDMSPYADQSIKVRISLSKALGDKAYEWNDNEMYLFRSSVAVAMROYFLKVK 660
 DB 601 NSFVGWSTDMSPYADQSIKVRISLSKALGDKAYEWNDNEMYLFRSSVAVAMROYFLKVK 660
 QY 661 QMILFGEEDVRVANLKPRISENFVFTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLND 720
 DB 661 QMILFGEEDVRVANLKPRISENFVFTAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLND 720
 QY 721 SLEFLGIQFTLGPNNQPPVSWLIVFGVGMVIVGIVLIFTGIRDRKKKKKARSGENP 780
 DB 721 SLEFLGIQFTLGPNNQPPVSWLIVFGVGMVIVGIVLIFTGIRDRKKKKKARSGENP 780
 QY 781 YASIDISKGENNPGFQNTDDVQTSF 805
 DB 781 YASIDISKGENNPGFQNTDDVQTSF 805
 XX
 XX RESULT 2
 XX AAY67310
 XX ID AAY67310 standard; Protein; 805 AA.
 XX
 XX AAY67310;
 XX AC
 XX 11-APR-2000 (first entry)
 XX
 XX Human MPROT15 amino acid sequence #1.
 XX
 XX MPROT15; treatment; hypertension; human; myocardial disease; apoplexy;
 XX heart disease; apoplexy; heart disease; nervous denaturation; hormone;
 XX Alzheimer's disease; cytokine.
 XX
 XX Homo sapiens.
 XX
 XX JPL1318472-A.
 XX
 XX 24-NOV-1999.
 XX
 XX 22-JAN-1999; 99JP-0014949.
 XX
 XX 13-MAY-1998; 98GB-0010373.
 XX
 XX 18-AUG-1998; 98GB-0018009.
 XX
 XX (SMIX) SMITHKLINE BEECHAM PLC.
 XX
 XX WPI; 2000-109268/10.
 XX
 XX N-PSDB; AA259465.
 XX
 XX MPROT15 polypeptide and MPROT15 polynucleotides - useful for the
 XX treatment of hypertension, myocardial diseases, apoplexy, heart
 XX diseases, nervous denaturation, Alzheimer's disease etc.
 XX
 XX Claim 1; Page 15; 22pp; Japanese.
 XX
 XX This is amino acid sequence #1 of human MPROT15. The MPROT15
 XX polynucleotide and polypeptide sequences can be used for the treatment of
 XX hypertension, myocardial diseases, apoplexy, heart diseases, nervous
 XX denaturation, Alzheimer's disease and diseases related to the processing
 XX of peptide hormones and cytokines.
 XX
 XX Sequence 805 AA;
 XX
 XX Query Match 100.0%; Score 4291; DB 21; Length 805;
 XX Best Local Similarity 100.0%; Pred. No. 0;
 XX Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
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 DB 1 MSSSSWLLSLVAVTAQSTIEEQAKTFLDKFNHEADLFYQSSLASWNTNITEENVQ 60

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QY 121 NTMSTIYGTGKVCNPDNPQECLELLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180
Db 121 NTMSTIYGTGKVCNPDNPQECLELLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180
QY 181 EYVVLKEMARANEHYEDYDYGWDYEVNGVDYDYSRGQLIEDVEHTFEELKPIYEH 240
Db 181 EYVVLKEMARANEHYEDYDYGWDYEVNGVDYDYSRGQLIEDVEHTFEELKPIYEH 240
QY 241 HAYVRAKLNNAYPSYISPIGCLPAHLGDMWGRFWNTNLYSLTFPGQKPNIDVTDAVDQ 300
Db 241 HAYVRAKLNNAYPSYISPIGCLPAHLGDMWGRFWNTNLYSLTFPGQKPNIDVTDAVDQ 300
QY 301 ANDAQRIFKEAEKFFVSGLPNMTQGFWENSMITDPGNVQKAVCHPTAWDLGKDFRILM 360
Db 301 ANDAQRIFKEAEKFFVSGLPNMTQGFWENSMITDPGNVQKAVCHPTAWDLGKDFRILM 360
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Db 361 CTYKVTMDLFLTAHMGHIQDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
QY 421 IGLSPDFQEDNETEINFLLQAALTIQVTLPTFTYMLEKRWMMVFKEIPKQOMMKWGM 480
Db 421 IGLSPDFQEDNETEINFLLQAALTIQVTLPTFTYMLEKRWMMVFKEIPKQOMMKWGM 480
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Db 481 KKEIVGVVEPVPHDITYCDPASLFRVSDYSFIRYITRTLYQFQFQALCOAAKHEGPLH 540
QY 541 KCDISNSTEAGOKLFNMLRLKSEFPWTLAENVVGAKNMVRPLLYFEPFLTWLKDQNK 600
Db 541 KCDISNSTEAGOKLFNMLRLKSEFPWTLAENVVGAKNMVRPLLYFEPFLTWLKDQNK 600
QY 601 NSFCWSTDMSPYADOSIKVRLSKALGDKAVENWNNEMVLPSSVAVAMRQYFLKVN 660
Db 601 NSFCWSTDMSPYADOSIKVRLSKALGDKAVENWNNEMVLPSSVAVAMRQYFLKVN 660
QY 661 QMILFGEEDVRVANLKPRISNFFVTAPKNVSDIIPRTEVEKAIKMSRINDAFLNDN 720
Db 661 QMILFGEEDVRVANLKPRISNFFVTAPKNVSDIIPRTEVEKAIKMSRINDAFLNDN 720
QY 721 SLEFLGIQPTLGPNNQPPVSLWLVGVWGVVGVVGVVGVVGVVGVVGVVGVVGVVGVV 780
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Db 781 YASIDISKGNPNPGFQNTDDVQTSF 805

RESULT 3
AAY72667
ID AAY72667 standard; Protein; 805 AA.
XX AC AAY72667;
XX DT 31-MAY-2001 (first entry)
XX DE Human angiotensin converting enzyme-2 (ACE-2).
XX KW Human; angiotensin converting enzyme-2; ACE-2; peptidyl dipeptidase A;
XX KW screening; therapy; hypertension; congestive heart failure; CHF;
XX KW inflammation; pain.
XX OS Homo sapiens.
XX FH Key
XX FT Peptide
XX FT Peptide
XX FT Protein

```

```

FT Domain
FT /label= Mature ACE-2 protein
FT 374..378
FT /label= ZBD
FT /note= "Zinc binding domain"
FT 741..765
FT /label= TMD
FT /note= "Transmembrane domain; Hydrophobic region"
FT 766..805
FT /label= Cytoplasmic_domain
XX US6194556-B1.
XX 27-FEB-2001.
XX 11-DEC-1997; 97US-0989299.
XX 11-DEC-1997; 97US-0989299.
XX (MILL-) MILLENNIUM PHARM INC.
XX Acton SL, Robison KE;
XX WPI; 2001-210604/21.
XX N-PSDB; AAD02758.
XX Novel genes encoding angiotensin converting enzyme-2 useful as
XX antisense or antigen agents for therapeutics, diagnostics and
XX screening assays.
XX Claim 33; Fig 1; 76pp; English.
XX The present amino acid sequence is human angiotensin converting enzyme-2
XX (ACE-2), also referred as peptidyl dipeptidase A (EC 3.4.15.1). Nucleic
XX acid sequence encoding ACE-2 is useful as antisense or antigen agents
XX for sequence specific modulation of gene expression or in the analysis of
XX single base-pair mutations in the gene. Nucleic acid sequence encoding
XX ACE-2 is useful in therapeutics, diagnostics and in screening assays.
XX ACE-2 antagonist is used to treat hypertension or congestive heart
XX failure (CHF). ACE agonist is used to reduce the inflammation and pain
XX resulting from an insect sting or bite, which was accompanied by an
XX injection of bradykinin. Anti-ACE-2 antibodies are used to monitor ACE-2
XX protein levels for determining the disease or condition associated with
XX an aberrant protein level.
XX Sequence 805 AA;

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Query Match 100.0%; Score 4291; DB 22; Length 805;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEADLFYQSSLASWNYNTNITEENVQ 60
Db 1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEADLFYQSSLASWNYNTNITEENVQ 60
QY 61 NNNAGDKWSAFLEKQSTLAQMYPIQETONITVKLQLOALQONGSSVLSDEKSKRLNTIL 120
Db 61 NNNAGDKWSAFLEKQSTLAQMYPIQETONITVKLQLOALQONGSSVLSDEKSKRLNTIL 120
QY 121 NTMSTIYGTGKVCNPDNPQECLELLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180
Db 121 NTMSTIYGTGKVCNPDNPQECLELLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLY 180
QY 181 EYVVLKEMARANEHYEDYDYGWDYEVNGVDYDYSRGQLIEDVEHTFEELKPIYEH 240
Db 181 EYVVLKEMARANEHYEDYDYGWDYEVNGVDYDYSRGQLIEDVEHTFEELKPIYEH 240
QY 241 HAYVRAKLNNAYPSYISPIGCLPAHLGDMWGRFWNTNLYSLTFPGQKPNIDVTDAVDQ 300
Db 241 HAYVRAKLNNAYPSYISPIGCLPAHLGDMWGRFWNTNLYSLTFPGQKPNIDVTDAVDQ 300
QY 301 ANDAQRIFKEAEKFFVSGLPNMTQGFWENSMITDPGNVQKAVCHPTAWDLGKDFRILM 360
Db 301 ANDAQRIFKEAEKFFVSGLPNMTQGFWENSMITDPGNVQKAVCHPTAWDLGKDFRILM 360

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QY 361 CTXVTMDDELTAHEMGHIQYDMAYAAQPFLLRNGANGFHEAVGEIMSLSAATPKHLKS 420
 Db 361 CTXVTMDDELTAHEMGHIQYDMAYAAQPFLLRNGANGFHEAVGEIMSLSAATPKHLKS 420
 QY 421 IGLSPDFQEDNETEINFLKQALTIIVGTLPFTYMLEKRWVVFKEIPKQWKKWEM 480
 Db 421 IGLSPDFQEDNETEINFLKQALTIIVGTLPFTYMLEKRWVVFKEIPKQWKKWEM 480
 QY 481 KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYTRTLTQFQOEALCOAAKHEGPLH 540
 Db 481 KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYTRTLTQFQOEALCOAAKHEGPLH 540
 QY 541 KCDISNSTEAGQKLFNNLRIGKSEPTLALENVGAKNNVRPLINYPEPFTLWKDQNK 600
 Db 541 KCDISNSTEAGQKLFNNLRIGKSEPTLALENVGAKNNVRPLINYPEPFTLWKDQNK 600
 QY 601 NSFVGMSTDSVPADQSIKVRISLKSALGDKAYENDNEMYLFRSSVAYAMQYFLKVKX 660
 Db 601 NSFVGMSTDSVPADQSIKVRISLKSALGDKAYENDNEMYLFRSSVAYAMQYFLKVKX 660
 QY 661 QMILFGEEDYRVANLKPRISENFVTPAKNVSIIIPRTEVEKAIIRMSRINDAFRLND 720
 Db 661 QMILFGEEDYRVANLKPRISENFVTPAKNVSIIIPRTEVEKAIIRMSRINDAFRLND 720
 QY 721 SLFELGIQPTLGPNNOPPVSIMLIVFGVGVVIVGIVLIFTGIRDRKKKARSGENP 780
 Db 721 SLFELGIQPTLGPNNOPPVSIMLIVFGVGVVIVGIVLIFTGIRDRKKKARSGENP 780
 QY 781 YASIDISKGNENPGQNTDDVQTSF 805
 Db 781 YASIDISKGNENPGQNTDDVQTSF 805

RESULT 4

AAB48095
 ID AAB48095 standard; Protein; 805 AA.

AC AAB48095;

DT 19-MAR-2001 (first entry)

DE Human Zace2 protein.

KW Zace2; metalloenzyme; angiotensin-converting enzyme; ACE; fertility;
 zinc metalloproteinase; blood pressure; zinc protease; hypertension;
 ventricular systolic dysfunction; renal impairment; heart failure;
 scleroderma renal crisis; atherosclerosis; antiinflammatory; human;
 antiarthritic; bradykinin inactivator.

OS Homo sapiens.

PN WO200070032-A1.

XX 23-NOV-2000.

PF 03-MAY-2000; 2000WO-US11932.

PR 13-MAY-1999; 99US-0311482.

PR 27-AUG-1999; 99US-0384706.

PA (ZYMO) ZYMOGENETICS INC.

PI Piddington CS, Petrie CR, Shoemaker KE, Bishop PD;

XX WPI; 2001-025018/03.

DR N-PSDB; AAC84366, AAC84367.

XX Angiotensin-converting enzyme, Zace2, useful for treating inflammatory
 bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases
 associated with inflammation such as arthritis and enterocolitis -

PS Example 1; Page 95-100; 125pp; English.

XX The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-
 converting enzyme is a zinc metalloproteinase that plays roles in blood
 pressure regulation and fertility. Zace2 can be expressed by standard
 recombinant methodology. Zace2 polypeptides are useful for treating an
 inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis),
 diseases associated with inflammation like arthritis and enterocolitis,
 as targets for identifying modulators of zinc protease activity, for
 screening or identifying new angiotensin-converting enzyme (ACE)
 inhibitors, and as a basis for rational drug design for inhibitory
 molecules. The nucleic acids can be used to detect the expression of a
 Zace2 gene in a biological sample, as probes for in vivo diagnosis and
 for detecting and localizing Zace2 gene expression in tissue samples,
 to determine whether a subject's chromosomes contain a mutation in the
 Zace2 gene, and to detect aberrations associated with the Zace2 locus.
 Inhibitors of ACE are used for treating hypertension of various
 conditions, including left ventricular systolic dysfunction, progressive
 renal impairment, scleroderma renal crisis, congestive heart failure due
 to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be
 used to treat infertility while Zace2 antagonists are used for inducing
 infertility. The present sequence represents the human Zace2 protein.
 XX Sequence 805 AA;

Query Match 100.0%; Score 4291; DB 22; Length 805;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSSSWLLLSLVATAAQSTIEQAKTFLDKFHEAEDLFYQSSLASWYNNYNTENVQ 60
 Db 1 MSSSSWLLLSLVATAAQSTIEQAKTFLDKFHEAEDLFYQSSLASWYNNYNTENVQ 60
 QY 61 NNNNAGDKWSAFLKEQSTLAQMYPLQBIQNLTKVLQALQALQNGSSVLSEKRLNTIL 120
 Db 61 NNNNAGDKWSAFLKEQSTLAQMYPLQBIQNLTKVLQALQALQNGSSVLSEKRLNTIL 120
 QY 121 NTMSTIYTGKVCNPDNPQECILLEPGLNEIMANSIDYNERLWAMESWSEVKGQLRPLY 180
 Db 121 NTMSTIYTGKVCNPDNPQECILLEPGLNEIMANSIDYNERLWAMESWSEVKGQLRPLY 180
 QY 181 EYVVLKNEMARANHYEDYDWRGDYEVNGVDGYDSRGQLIETVEHTFEIKPLYEHL 240
 Db 181 EYVVLKNEMARANHYEDYDWRGDYEVNGVDGYDSRGQLIETVEHTFEIKPLYEHL 240
 QY 241 HAYVRAKLMWAPSYISPIGCLPAHLGDMWGFNTNLYSLTVPFGKPNIDVTAMDQ 300
 Db 241 HAYVRAKLMWAPSYISPIGCLPAHLGDMWGFNTNLYSLTVPFGKPNIDVTAMDQ 300
 QY 301 AWDAQRIFKEAEKFPVSVGLPNNMTQGFWNSMLTDFGNVQKAVCHPTAMDLGKGFRIIM 360
 Db 301 AWDAQRIFKEAEKFPVSVGLPNNMTQGFWNSMLTDFGNVQKAVCHPTAMDLGKGFRIIM 360
 QY 361 CTKVTMDDELTAHEMGHIQYDMAYAAQPFLLRNGANGFHEAVGEIMSLSAATPKHLKS 420
 Db 361 CTKVTMDDELTAHEMGHIQYDMAYAAQPFLLRNGANGFHEAVGEIMSLSAATPKHLKS 420
 QY 421 IGLSPDFQEDNETEINFLKQALTIIVGTLPFTYMLEKRWVVFKEIPKQWKKWEM 480
 Db 421 IGLSPDFQEDNETEINFLKQALTIIVGTLPFTYMLEKRWVVFKEIPKQWKKWEM 480
 QY 481 KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYTRTLTQFQOEALCOAAKHEGPLH 540
 Db 481 KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYTRTLTQFQOEALCOAAKHEGPLH 540
 QY 541 KCDISNSTEAGQKLFNNLRIGKSEPTLALENVGAKNNVRPLINYPEPFTLWKDQNK 600
 Db 541 KCDISNSTEAGQKLFNNLRIGKSEPTLALENVGAKNNVRPLINYPEPFTLWKDQNK 600
 QY 601 NSFVGMSTDSVPADQSIKVRISLKSALGDKAYENDNEMYLFRSSVAYAMQYFLKVKX 660
 Db 601 NSFVGMSTDSVPADQSIKVRISLKSALGDKAYENDNEMYLFRSSVAYAMQYFLKVKX 660
 QY 661 QMILFGEEDYRVANLKPRISENFVTPAKNVSIIIPRTEVEKAIIRMSRINDAFRLND 720

661 QMLGGEEDVAVANLKPRISNFFVTAPOKNSDIIPTEVEKAIMRSRINDAFRLNDN 720
 721 SLEFGLIGIOTLGPQPPVSVLWLVFVGMGVVGVVILFTGIRDKKKNKARSGENP 780
 721 SLEFGLIGIOTLGPQPPVSVLWLVFVGMGVVGVVILFTGIRDKKKNKARSGENP 780
 781 YASIDISKGNPNPGFQNTDDVQTSF 805
 781 YASIDISKGNPNPGFQNTDDVQTSF 805
 RESULT 5
 ABG77011
 ID ABG77011 standard; Protein; 805 AA.
 AC ABG77011;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Human angiotensin converting enzyme 2.
 XX
 KW Aminopeptidase P; XNPEP2; bradykinin receptor B1;
 KW BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;
 KW kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
 KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
 KW cardiovascular disease; angina pectoris; hypertension; heart failure;
 KW myocardial infarction; ventricular hypertrophy; vascular disease;
 KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
 KW autoimmune disease; inflammatory arthritis; cancer; wound;
 KW viral infection; bacterial infection; fungal infection; COPD;
 KW Chronic obstructive pulmonary disease; enterocolitis.
 XX
 OS Homo sapiens.
 XX
 XX WO200261131-A2.
 XX
 XX 09-AUG-2002.
 XX
 XX 03-DEC-2001; 2001WO-US47235.
 XX
 XX 04-DEC-2000; 2000US-251015P.
 XX 23-JAN-2001; 2001US-263678P.
 XX 02-MAR-2001; 2001US-273037P.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX (TSUC/) TSUCHIHASHI Z.
 XX (HUI/L) HUI L.
 XX
 XX Tauchihasi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
 XX Swanson BN, Powell JR;
 XX
 XX WPI; 2002-619265/66.
 XX N-PSDB; ABS60372.
 XX
 XX New isolated nucleic acid with at least one polymorphic position,
 XX useful for detecting, diagnosing and treating disorders such as
 XX angioedema, cancer, viral, bacterial or fungal infection,
 XX cardiovascular and autoimmune diseases -
 XX
 XX Disclosure; Fig 32; 977pp; English.
 XX
 XX The invention relates to an isolated nucleic acid from a human gene
 XX encoding aminopeptidase P (XNPEP2), bradykinin receptor B1 (BDKRB1),
 XX tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
 XX 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
 XX 2 (ACE2) or protease inhibitor 4 (P14), comprising at least one
 XX polymorphic position. Also included are (1) a probe that hybridises to a
 XX polymorphic position as provided in the detailed summary of single
 XX nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
 XX sequence; (2) analysing (M1) at least one nucleic acid sample comprising

obtaining the sample from one or more individuals and determining the
 nucleic acid sequence at one or more polymorphic positions in a gene
 encoding a protein selected from the group above; (3) constructing (M2)
 haplotypes using the genes comprising grouping at least two nucleic
 acids; (4) identifying (M3) an individual at risk of developing a
 disorder upon administration of an ACE inhibitor and/or vasopeptidase
 inhibitor using the polymorphic data; (5) a library of nucleic acids,
 each of which comprises one or more polymorphic positions within a gene
 encoding a human protein selected from the group above; and (6)
 genotyping (M4) an individual comprising obtaining a nucleic acid sample,
 and comparing the nucleotide present in at least one polymorphic position,
 and comparing at least one position with a known data set. The genes,
 (M1, M2, M3 and M4) and compositions are useful for detecting,
 diagnosing, treating, preventing various disorders such as angioedema
 and diseases which involve angiogenesis like haemangiomas, tumours,
 sarcomas, Crohn's disease, trachoma, and cardiovascular diseases like
 angina pectoris, hypertension, heart failure, myocardial infarction,
 ventricular hypertrophy, vascular diseases, aneurysm, embolism,
 thrombosis, coronary artery disease, arteriosclerosis and/or
 atherosclerosis, and hypersensitivity reactions, sepsis, autoimmune
 diseases, inflammatory arthritis, cancer, wounds, viral, bacterial or
 fungal infection, chronic obstructive pulmonary disease (COPD) and
 enterocolitis (many other diseases and disorders are listed in the
 specification). The polymorphisms are also useful for chromosome
 identification. Antibodies against the proteins may be utilised for
 immunophenotyping of cell lines and biological samples. The present
 sequence represents one of the proteins listed above.
 XX
 XX Sequence 805 AA;
 XX
 Query Match 100.0%; Score 4291; DB 23; Length 805;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSSSSWLLLSLVAVTAQAQSTIEBOAKTFELDKFNHAEADLFYQSSLASWYNTNITEENVQ 60
 DB 1 MSSSSWLLLSLVAVTAQAQSTIEBOAKTFELDKFNHAEADLFYQSSLASWYNTNITEENVQ 60
 QY 61 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTKLOLQALQNGSSVLSDESKRLNTLL 120
 DB 61 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTKLOLQALQNGSSVLSDESKRLNTLL 120
 QY 121 NTMSTIYSTGKVCNPNPQECLELLEPGLNEIMANSIDYNERLWAWESWSEVKGKQLRPLY 180
 DB 121 NTMSTIYSTGKVCNPNPQECLELLEPGLNEIMANSIDYNERLWAWESWSEVKGKQLRPLY 180
 QY 181 EYVVLKXENARANHEDYDGYWRGDYEVNGVDGYDYSRGQIEDVEHTFEEIKPLYEHL 240
 DB 181 EYVVLKXENARANHEDYDGYWRGDYEVNGVDGYDYSRGQIEDVEHTFEEIKPLYEHL 240
 QY 241 HAYVRKLMNAYPSYISPIGCLPAHLLDGMWGFNTNLSLTVPFQCKENIDVTDAMVDQ 300
 DB 241 HAYVRKLMNAYPSYISPIGCLPAHLLDGMWGFNTNLSLTVPFQCKENIDVTDAMVDQ 300
 QY 301 AWDAQRIFKBAEKFFVSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRLIM 360
 DB 301 AWDAQRIFKBAEKFFVSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRLIM 360
 QY 361 CTKVTMDDFLTAHHEMGHIQYDMAYAAQAPFLRNGANEGFHEAVGIMSLSAATPHLKS 420
 DB 361 CTKVTMDDFLTAHHEMGHIQYDMAYAAQAPFLRNGANEGFHEAVGIMSLSAATPHLKS 420
 QY 421 IGLLSPPQEDNETEINFILKQALITVGTLPFFYMLKRWVFWFKGEIPKQDKMKNWEM 480
 DB 421 IGLLSPPQEDNETEINFILKQALITVGTLPFFYMLKRWVFWFKGEIPKQDKMKNWEM 480
 QY 481 KREIVGVVPEVPHDETCDPASLFHVSNDYSFIRYTRTLTYQFQFQALCOAKHEGPHLH 540
 DB 481 KREIVGVVPEVPHDETCDPASLFHVSNDYSFIRYTRTLTYQFQFQALCOAKHEGPHLH 540
 QY 541 KCDISNSTEAGOKLFNMLRKGSEPTALENVVGAKNMVRPLNYPFPLFTWLKDQNK 600
 DB 541 KCDISNSTEAGOKLFNMLRKGSEPTALENVVGAKNMVRPLNYPFPLFTWLKDQNK 600

QY 601 NSFVGSWTDNSPYADQSIKVRISLKSALGDKAYENDNEMYLPRSSVAVAMEQYFLKYN 660
 Db 601 NSFVGSWTDNSPYADQSIKVRISLKSALGDKAYENDNEMYLPRSSVAVAMEQYFLKYN 660
 QY 661 QMILFGEEDVRANLKRISFNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFLNDN 720
 Db 661 QMILFGEEDVRANLKRISFNFFVTAPKNVSDIIPRTEVEKAIKMSRSRINDAFLNDN 720
 QY 721 SLERLGIOTPLGPNOPVSWLIVFGVWGVWGIIVLIFGIDRCKKAKSGENP 780
 Db 721 SLERLGIOTPLGPNOPVSWLIVFGVWGVWGIIVLIFGIDRCKKAKSGENP 780
 QY 781 YASIDISKGENNPGFQNTDDVQTSF 805
 Db 781 YASIDISKGENNPGFQNTDDVQTSF 805

RESULT 5

ABG77023

ID ABG77023 standard; Protein; 805 AA.

XX AC ABG77023;

XX DT 05-NOV-2002 (first entry)

XX Human angiotensin converting enzyme 2 variant #1.

XX Aminopeptidase P; XNBP2; bradykinin receptor B1; human;

XX BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;

XX kallikrein 1; KUK1; bradykinin receptor B2; BDKRB2; gene therapy;

XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;

XX polymorphisms; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;

XX cardiovascular disease; angina pectoris; hypertension; heart failure;

XX myocardial infarction; ventricular hypertrophy; vascular disease;

XX aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;

XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;

XX autoimmune disease; inflammatory arthritis; cancer; wound;

XX viral infection; bacterial infection; fungal infection; COPD;

XX Chronic obstructive pulmonary disease; enterocolitis.

XX Homo sapiens.

XX WO200261131-A2.

XX 08-AUG-2002.

XX 03-DEC-2001; 2001WO-US47235.

XX 04-DEC-2000; 2000US-251015P.

XX 23-JAN-2001; 2001US-263678P.

XX 02-MAR-2001; 2001US-273037P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX (TSUC/) TSUCHIHASHI Z.

XX (HUI/) HUI L.

XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;

XX Swanson BN, Powell JR;

XX N-PSDB; ABS60633.

XX WPI; 2002-619265/66.

XX New isolated nucleic acid with at least one polymorphic position,

XX useful for detecting, diagnosing and treating disorders such as

XX angioedema, cancer, viral, bacterial or fungal infection,

XX cardiovascular and autoimmune diseases -

XX Disclosure; Fig 37; 977pp; English.

XX The invention relates to an isolated nucleic acid from a human gene

XX encoding aminopeptidase P (XNBP2), bradykinin receptor B1 (BDKRB1),

XX tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein

CC 1 (KUK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
 CC 2 (ACE2) or protease inhibitor 4 (P14), comprising at least one
 CC polymorphic position. Also included are (1) a probe that hybridises to a
 CC polymorphic position as provided in the detailed summary of single
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
 CC obtaining the sample from one or more individuals and determining the
 CC nucleic acid sequence at one or more polymorphic positions in a gene
 CC encoding a protein selected from the group above; (3) constructing (M2)
 CC haplotypes using the genes comprising grouping at least two nucleic
 CC acids; (4) identifying (M3) an individual at risk of developing a
 CC disorder upon administration of an ACE inhibitor and/or vasopeptidase
 CC inhibitor using the polymorphic data; (5) a library of nucleic acids,
 CC each of which comprises one or more polymorphic positions within a gene
 CC encoding a human protein selected from the group above; and (6)
 CC genotyping (M4) an individual comprising obtaining a nucleic acid sample,
 CC determining the nucleotide present in at least one polymorphic position,
 CC and comparing at least one position with a known data set. The genes,
 CC (M1, M2, M3 and M4) and compositions are useful for detecting,
 CC diagnosing, treating, preventing various disorders such as angiodaema
 CC and diseases which involve angiogenesis like haemangiomas, tumours, and
 CC sarcomas, Crohn's disease, trachomas, and cardiovascular diseases like
 CC angina pectoris, hypertension, heart failure, myocardial infarction,
 CC ventricular hypertrophy, vascular diseases, aneurysm, embolism,
 CC thrombosis, coronary artery disease, arteriosclerosis and/or
 CC atherosclerosis, and hypersensitivity reactions, sepsis, autoimmune
 CC diseases, inflammatory arthritis, cancer, wounds, viral, bacterial or
 CC fungal infection, Chronic obstructive pulmonary disease (COPD) and
 CC enterocolitis (many other diseases and disorders are listed in the
 CC specification). The polynucleotides are also useful for chromosome
 CC identification. Antibodies against the proteins may be utilised for
 CC immunophenotyping of cell lines and biological samples. The present
 CC sequence represents a polymorphic variant of one of the proteins listed
 CC above.

XX SQ Sequence 805 AA;

Query Match 100.0%; Score 4291; DB 23; Length 805;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEADLFYQSSLASWYNTNITEENVQ 60

Db 1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEADLFYQSSLASWYNTNITEENVQ 60

QY 61 NVNNAQKWSAFLKEOSTLAQMYELOIQLTVKLOALQONGSSVLGDKSKRLNTIL 120

Db 61 NVNNAQKWSAFLKEOSTLAQMYELOIQLTVKLOALQONGSSVLGDKSKRLNTIL 120

QY 121 NTMSTIYTGKVCNPDNPQECCLLEPGLNEIMANSLDYNERLWAWESWSEVGKQLRPLY 180

Db 121 NTMSTIYTGKVCNPDNPQECCLLEPGLNEIMANSLDYNERLWAWESWSEVGKQLRPLY 180

QY 181 EYVVLKNEMARANHYEDYGDYWGVEVNGVDGYDSRGOLLEDVEHTFEELKPLYEHL 240

Db 181 EYVVLKNEMARANHYEDYGDYWGVEVNGVDGYDSRGOLLEDVEHTFEELKPLYEHL 240

QY 241 HAYVRAKLMNAYPSYISPGICLPAHLGDMGRFNTNLSYLTVPFGCKNIDVTDAMVQ 300

Db 241 HAYVRAKLMNAYPSYISPGICLPAHLGDMGRFNTNLSYLTVPFGCKNIDVTDAMVQ 300

QY 301 AMDAQRIFKEAEKFPVSVGLPNMTQGWENSMITDPGNVQKAVCHPTAMDGLGDFRILM 360

Db 301 AMDAQRIFKEAEKFPVSVGLPNMTQGWENSMITDPGNVQKAVCHPTAMDGLGDFRILM 360

QY 361 CTKVMTDDFLTAHEMGIHQYDMAAQAQPFLLNGANEHGAHVGBMSLSAATPKHLKS 420

Db 361 CTKVMTDDFLTAHEMGIHQYDMAAQAQPFLLNGANEHGAHVGBMSLSAATPKHLKS 420

QY 421 IGLLSPDQEDNETEINFLLKQALTVGTLPFTYMLEKWRVMVFKGEIPKQDMKKWWM 480

Db 421 IGLLSPDQEDNETEINFLLKQALTVGTLPFTYMLEKWRVMVFKGEIPKQDMKKWWM 480

QY 481 KKEIVGVVEPVDHETCDPASLPHVSNDSYFIRYTYRTLYQFOQALCOAAKHGEPHL 540
 Db 481 KKEIVGVVEPVDHETCDPASLPHVSNDSYFIRYTYRTLYQFOQALCOAAKHGEPHL 540
 QY 541 KCDISNSTEAGQKLFNMLRLGKSEPTLALENVVGAKNMVRPLNTYFELFTWLKDQNK 600
 Db 541 KCDISNSTEAGQKLFNMLRLGKSEPTLALENVVGAKNMVRPLNTYFELFTWLKDQNK 600
 QY 601 NSFVGSWSDWSPYADQSIKVRISLKSALGDKAYEWNDNEMYLPRSSVAYAMROVFLKVKX 660
 Db 601 NSFVGSWSDWSPYADQSIKVRISLKSALGDKAYEWNDNEMYLPRSSVAYAMROVFLKVKX 660
 QY 661 QMILFGEEDVRVANLKPISNFFVTAPKNVSDIIPRTEVEKALRMGRSINDAFLNDN 720
 Db 661 QMILFGEEDVRVANLKPISNFFVTAPKNVSDIIPRTEVEKALRMGRSINDAFLNDN 720
 QY 721 SLEFLGIGTLPFPNPQPVSIWLVFGVMGVIVVGVIVLIFTGIRDKKKKARGSENP 780
 Db 721 SLEFLGIGTLPFPNPQPVSIWLVFGVMGVIVVGVIVLIFTGIRDKKKKARGSENP 780
 QY 781 YASIDISKGNPNPQNTDDVQTSF 805
 Db 781 YASIDISKGNPNPQNTDDVQTSF 805

RESULT 7
 AAU99701
 ID AAU99701 standard; Protein; 805 AA.
 AC AAU99701;
 XX
 DT 24-SEP-2002 (first entry)
 XX
 DE Human angiotensin converting enzyme-2 (ACE-2) protein.
 XX
 KW Human; angiotensin converting enzyme-2; ACE-2; body weight disorder;
 KW muscle mass; body fat; obesity; diabetes; atherosclerosis; weight loss;
 KW lipid metabolism; weight gain; anorexia; cachexia; bulimia; sepsis;
 KW familial partial lipodystrophy; hypercholesterolaemia; hyperlipidaemia;
 KW aberrant metabolic rate; heart failure; left ventricular hypertrophy;
 KW neurodegenerative disorder; peptide hormone; cytokine processing;
 KW myocardial infarction; cardiomyopathy; inflammatory bowel disease;
 KW systemic inflammation response syndrome; polytrauma; pain; stroke;
 KW bone destruction; rheumatoid arthritis; osteoarthritis; asthma;
 KW periodontal disease; dysmenorrhea; premature labour; brain oedema;
 KW focal injury; diffuse axonal injury; reperfusion injury; scar formation;
 KW cerebral vasospasm; subarachnoid haemorrhage; allergic disorder;
 KW adult respiratory distress syndrome; wound healing; appetite;
 KW body mass index.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FH Location/Qualifiers
 FT Peptide
 FT 1..19
 FT /label= Signal_peptide
 FT Protein
 FT 19..805
 FT /label= Mature_human_ACE_2_protein
 XX
 PN WC020239997-A2.
 XX
 PD 23-MAY-2002.
 XX
 PF 31-OCT-2001; 2001WO-US45703.
 XX
 PR 01-NOV-2000; 2000US-0704216.
 PR 29-MAY-2001; 2001US-0870382.
 PR 19-OCT-2001; 2001US-371741P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Acton SL, Ocain TD, Gould AE, Dales NA, Guan B, Brown JA;
 PI Patane M, Kadambi VU, Solomon M, Stricker-Krongrad A;
 XX

DR WPI: 2002-547572/58.
 XX N-PSDB; ABK87623.
 PT Treating body weight disorder and increasing muscle mass comprises
 XX administering angiotensin converting enzyme-2 modulating compound -
 PS Example 5; Page 387-390; 395pp; English.
 XX
 CC The present invention describes a new method of treating a body weight
 CC disorder, increasing muscle mass and decreasing body fat by
 CC administration of angiotensin converting enzyme (ACE)-2 modulating
 CC compound. The invention can be used for treating body weight disorders,
 CC particularly obesity of at least grade 1, diabetes, atherosclerosis and
 CC a state associated with lipid metabolism. The method is used for treating
 CC rapid weight loss, rapid weight gain, anorexia, cachexia, bulimia,
 CC generalised partial lipodystrophy, familial partial lipodystrophy,
 CC hypercholesterolaemia, hyperlipidaemia, an aberrant metabolic rate,
 CC congestive heart failure, chronic heart failure, left ventricular
 CC hypertrophy, acute heart failure, neurodegenerative disorders (e.g.
 CC Alzheimer's disease, Parkinson's disease and Huntington's disease),
 CC diseases associated with peptide hormones or cytokine processing,
 CC myocardial infarction, cardiomyopathy, systemic inflammation response
 CC syndrome, sepsis, polytrauma, inflammatory bowel disease, acute and
 CC chronic pain, bone destruction in rheumatoid arthritis and osteoarthritis
 CC and periodontal disease, dysmenorrhea, premature labour, brain oedema
 CC following focal injury, diffuse axonal injury, stroke, reperfusion
 CC injury, cerebral vasospasm after subarachnoid haemorrhage, allergic
 CC disorders including asthma, adult respiratory distress syndrome, wound
 CC healing and scar formation. The invention decreases the appetite, wound
 CC increases muscle mass and decreases body fat of subject having body mass
 CC index of greater than 23 (preferably 24.9kg/m²). The present amino
 CC acid sequence represents the human ACE-2 protein of the invention.
 XX
 SQ Sequence 805 AA;
 Query Match 100.0%; Score 4291; DB 23; Length 805;
 Seq. Local Similarity 100.0%; Pred. No. 0;
 Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSSSSLLLSLVATAAQAQSTIEQAKTFDKFNHEADLFYQSSLSAMWNTNTEENVQ 60
 Db 1 MSSSSLLLSLVATAAQAQSTIEQAKTFDKFNHEADLFYQSSLSAMWNTNTEENVQ 60
 QY 61 MNMAGDKSAFLKEQSTLAQMPLOEIQNLTKVLQALQNGSSVLSEDSKRLNTIL 120
 Db 61 MNMAGDKSAFLKEQSTLAQMPLOEIQNLTKVLQALQNGSSVLSEDSKRLNTIL 120
 QY 121 NTMTIYSTGKVCNPNPQSCILLLEPCLNEIMANSLDYNERLWAMESWSEVKGQLRPLY 180
 Db 121 NTMTIYSTGKVCNPNPQSCILLLEPCLNEIMANSLDYNERLWAMESWSEVKGQLRPLY 180
 QY 181 EYVVLKNEMARANHYEDYDGYWRGVDYVNGVDYSGQLIEDVEHFTFEIKPLYEHL 240
 Db 181 EYVVLKNEMARANHYEDYDGYWRGVDYVNGVDYSGQLIEDVEHFTFEIKPLYEHL 240
 QY 241 HAYVRAKLMNAYPSYISPIGCLPAHLGLDMWGFNTNLSLTVPPQCKNIDVTDAMVDQ 300
 Db 241 HAYVRAKLMNAYPSYISPIGCLPAHLGLDMWGFNTNLSLTVPPQCKNIDVTDAMVDQ 300
 QY 301 AWDAQRIFKEAEKFFVSVGLPNMTQGFWNSMLTDGPNVQKAVCHPTANDLKGDFRILM 360
 Db 301 AWDAQRIFKEAEKFFVSVGLPNMTQGFWNSMLTDGPNVQKAVCHPTANDLKGDFRILM 360
 QY 361 CTKYTMDDFLTATHEMGHIQYDMAYAAQPFLLNGANEGFHEAVGIMSLSAATPKHLKS 420
 Db 361 CTKYTMDDFLTATHEMGHIQYDMAYAAQPFLLNGANEGFHEAVGIMSLSAATPKHLKS 420
 QY 421 IGLLSPDFQEDNETEINFLKQALITVGTLPFTYMLEKRWVMVFKGEIPKDWMMKWMEM 480
 Db 421 IGLLSPDFQEDNETEINFLKQALITVGTLPFTYMLEKRWVMVFKGEIPKDWMMKWMEM 480
 QY 481 KREIVGVVEPVDHETCDPASLPHVSNDSYFIRYTYRTLYQFOQALCOAAKHGEPHL 540

Db 781 YASIDISKGENNPGFQNTDDVQISF 805

RESULT 9

ASU07731
ID ABU07731 standard; Protein; 805 AA.

AC ABU07731;

DT 27-MAY-2003 (first entry)

DE Human zinc metalloproteinase Zace2.

XX Human; enzymes; Zace2; zinc metalloproteinase; ulcerative colitis;
XX inflammation; inflammatory bowel disease; arthritis; enterocolitis;
XX Crohn's disease; gene therapy; transgenic.

OS Homo sapiens.

XX Key Location/Qualifiers
XX Region 371..380
XX /label= Expanded_zinc_binding_region
XX Region 374..378
XX /label= Zinc-binding_motif
XX Domain 739..761
XX /label= Transmembrane_domain

XX US200217211-A1.

XX 28-NOV-2002.

XX 16-OCT-2001; 2001US-0978385.

XX 13-MAY-1999; 99US-133952P.

XX 27-AUG-1999; 99US-151181P.

XX 03-MAY-2000; 2000US-0563516.

XX (ZYMO) ZYMOGENETICS INC.

XX Fiddington CS, Petrie C, Shoemaker KE, Bishop PD;

XX WPI; 2003-328489/31.

XX N-PSDB; ABX93333.

XX Isolated human or murine Zace2 polypeptide useful for reducing
XX inflammation in conditions such as inflammatory bowel disease,
XX arthritis, enterocolitis, ulcerative colitis and Crohn's disease

XX Claim 1; Page 39-41; 57pp; English.

XX The invention relates to an isolated polypeptide, comprising fully
XX defined human Zace2, murine Zace-5, or murine Zace2-10 polypeptide. An
XX expression vector containing Zace2 polynucleotide is useful for producing
XX Zace2 protein. The polynucleotide is useful as a diagnostic probe for
XX detecting a product of Zace2 gene expression in a biological sample. The
XX polypeptide is also useful for decreasing inflammation associated with a
XX condition such as inflammatory bowel disease, arthritis or enterocolitis.
XX The polypeptide is also useful for treating Crohn's disease and
XX ulcerative colitis. The polypeptide is useful for producing labelled
XX angiotensin II, for identifying modulators of zinc protease activity and
XX for identifying angiotensin converting enzyme (ACE) inhibitors. The
XX polynucleotide is useful in gene therapy techniques to treat the above
XX mentioned disorders. The polynucleotide is also useful for determining
XX whether a subject's chromosome contains a mutation in the Zace2 gene. The
XX present sequence represents the amino acid sequence of human zinc
XX metalloproteinase Zace2.

XX Sequence 805 AA;

XX Query Match 100.0%; Score 4291; DB 24; Length 805;
XX Best Local Similarity 100.0%; Pred. NO. 0;
XX Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSSSWLLLSLVAVTAAQSTIEOAKTFLDKFNHEAEDLFYCSSLASWNYNTNTEENVQ 60
DB 1 MSSSSWLLLSLVAVTAAQSTIEOAKTFLDKFNHEAEDLFYCSSLASWNYNTNTEENVQ 60
QY 61 NMNAGDKWSAFLEKQSTLAQMYPIQETONLTVKLQALQONGSSVLSSEKSLRNLIL 120
DB 61 NMNAGDKWSAFLEKQSTLAQMYPIQETONLTVKLQALQONGSSVLSSEKSLRNLIL 120
QY 121 NTMSTIYSTGKVCNPDNPQECCLLEPGLNEIMANSLDYNERLWAWESWRSSEVQKRLPLY 180
DB 121 NTMSTIYSTGKVCNPDNPQECCLLEPGLNEIMANSLDYNERLWAWESWRSSEVQKRLPLY 180
QY 181 EYVVLKNEANRANHYEDYDWRGVDYGVGVDYSGOLIEDVEHTEHTEHLEHL 240
DB 181 EYVVLKNEANRANHYEDYDWRGVDYGVGVDYSGOLIEDVEHTEHTEHLEHL 240
QY 241 HAYVRAKLANAYPSYISPIGCLPAHLGDMGRFWTNLYSLTVPGQKENDVTDAMVDQ 300
DB 241 HAYVRAKLANAYPSYISPIGCLPAHLGDMGRFWTNLYSLTVPGQKENDVTDAMVDQ 300
QY 301 AWDAQRIFEAEKFFVSVCLPNTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRLM 360
DB 301 AWDAQRIFEAEKFFVSVGLPNTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGFRLM 360
QY 361 CTKVTMDDELTAHHEMGHIQYDMAVAAQFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
DB 361 CTKVTMDDELTAHHEMGHIQYDMAVAAQFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
QY 421 IGLLSPDFQEDNETEINFLKQALTVIGLPTMYLKKRWNVFKEI PKDQMKKQWEM 480
DB 421 IGLLSPDFQEDNETEINFLKQALTVIGLPTMYLKKRWNVFKEI PKDQMKKQWEM 480
QY 481 KREIVGVWEPVPHDETYCDPASLHVSNDSYIRIYTRTLYQFQFQALCOAAKHEGSLH 540
DB 481 KREIVGVWEPVPHDETYCDPASLHVSNDSYIRIYTRTLYQFQFQALCOAAKHEGSLH 540
QY 541 KCDISNSTEAGOKLFNMLRGKSEPTLALENVGAKNNVRPLLYNYPELFTWLKQNK 600
DB 541 KCDISNSTEAGOKLFNMLRGKSEPTLALENVGAKNNVRPLLYNYPELFTWLKQNK 600
QY 601 NSFVGMSTDSWSPYADQSIKVRISLSKALGDKAYEWNENYLFSSVAYAYQVFLKYKN 660
DB 601 NSFVGMSTDSWSPYADQSIKVRISLSKALGDKAYEWNENYLFSSVAYAYQVFLKYKN 660
QY 661 QMLFGEEDVRVANLKPRISENFVFTAPKNVSDIIPRIEVEKAIKMSRSRINDAFRLND 720
DB 661 QMLFGEEDVRVANLKPRISENFVFTAPKNVSDIIPRIEVEKAIKMSRSRINDAFRLND 720
QY 721 SLEFLGIQPTLGPPOPPVSIWLIIVGVVMGVIVVGVIVILIFTGIRDRKKKARSGENP 780
DB 721 SLEFLGIQPTLGPPOPPVSIWLIIVGVVMGVIVVGVIVILIFTGIRDRKKKARSGENP 780
QY 781 YASIDISKGENNPGFQNTDDVQTSF 805
DB 781 YASIDISKGENNPGFQNTDDVQTSF 805

RESULT 10

AAU09092

ID AAU09092 standard; Protein; 711 AA.

XX AC AAU09092;

XX DT 20-DEC-2001 (first entry)

XX DE Novel human protein NHP #1.

XX Human; novel human protein; NHP; antidiabetic; antirheumatic;
XX antiarthritic; cytostatic; antiarteriosclerotic; vulnerary;
XX neuroprotective; nootropic; antiparkinsonian;
XX anti-human immunodeficiency virus; antiaesthatic; vasotropic; cardiant;
XX hypotensive; anorectic; antiinfertility; neuroleptic; anticonvulsant;

KW antinemic; immunosuppressive; cerebroprotective; antimicrobial;
 KW antiinflammatory; antibacterial; antipsoriatic; thyromimetic;
 KW immunomodulator; antiseborrheic; dermatological; vasoconstriction;
 KW gastrointestinal disorder; cardiovascular disorder; hypertension;
 KW coronary heart disease; arteriosclerosis; anorexia; obesity; bulimia;
 KW cachexia; male infertility; impotence; testicular cancer; lung tumour;
 KW hyperproliferative disorder; pulmonary system disorder;
 KW central nervous system disorder; bone disorder;
 KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; schizophrenia; mania; dementia; paranoia;
 KW panic disorder; learning disability; anyotropic lateral sclerosis;
 KW psychosis; autism; sleep disorder; immune system disorder;
 KW Hashimoto's thyroiditis; musculo-skeletal system disorders;
 KW multiple sclerosis; ischemic brain injury; stroke; infectious disease;
 KW diabetes mellitus; immunological disorder; asthma; AIDS; immunogen;
 KW acquired immunodeficient syndrome; leukaemia; rheumatoid arthritis;
 KW inflammatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus;
 KW neural system disorder; respiratory disorder; olfactory disorder;
 KW wound healing; chromosome X.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..691
 FT /label= Extracellular_domain
 FT Region 48..55
 FT /label= Immunogenic_epitope
 FT Region 110..118
 FT /label= Immunogenic_epitope
 FT Region 136..146
 FT /label= Immunogenic_epitope
 FT Region 151..158
 FT /label= Immunogenic_epitope
 FT Misc-difference 219
 FT /label= OTHER
 FT /note= "Other= Any amino acid encoded by WST"
 FT Misc-difference 240
 FT /label= OTHER
 FT /note= "Other= Any amino acid encoded by RCC"
 FT Misc-difference 499
 FT /label= OTHER
 FT /note= "Other= Any amino acid encoded by NTT"
 FT Domain 682..698
 FT /label= Transmembrane_domain
 XX WO200174896-A1.
 XX
 XX 11-OCT-2001.
 XX
 XX 02-APR-2001; 2001WO-US10542.
 XX
 XX 03-APR-2000; 2000US-194118P.
 XX
 XX 29-SEP-2000; 2000US-236384P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Moore PA, Mi J, Soppet DR, Coleman TA, Gentz RL, Endress GA;
 XX Li Y, Dillon RJ;
 XX
 XX WPI; 2001-626394/72.
 XX
 XX N-PSDB; AAS14880.
 XX
 XX New human proteins, useful for diagnosing, treating, preventing and/or
 XX prognosing disorders related to the proteins, including cardiovascular
 XX disorders, autoimmune disorders and reproductive disorders -
 XX
 XX Claim 11; Page 298-301; 318pp; English.
 XX
 XX The invention relates to novel human proteins (NHP) and the
 XX nucleic acids that encode them and antibodies raised against them.
 XX The proteins, antibodies and nucleic acids are useful in the diagnosis,
 XX prognosis, prevention and/or treatment of diseases and/or disorders
 XX involving vasoconstriction, gastrointestinal disorders, cardiovascular

CC disorders (e.g. hypertension, erectile dysfunction, high blood pressure,
 CC coronary heart disease and arteriosclerosis), anorexia, obesity, bulimia,
 CC cachexia, disorders of small intestine, disorders of reproductive system
 CC (e.g. male infertility and/or impotence), testicular cancer, lung tumours
 CC and other hyperproliferative disorders, disorders of pulmonary system,
 CC central nervous system disorders, bone disorders, neurodegenerative
 CC diseases and behavioural disorders (e.g. Alzheimer's disease, Parkinson's
 CC disease, Huntington's disease, schizophrenia, mania, dementia, paranoia,
 CC panic disorder, learning disabilities, anyotropic lateral sclerosis,
 CC psychoses, autism, sleep disorders), immune system disorders (e.g.
 CC Hashimoto's thyroiditis), renal and musculo-skeletal system disorders,
 CC central nervous system disorders (e.g. multiple sclerosis, ischemic
 CC brain injury and/or stroke), infectious diseases, diabetes mellitus,
 CC immunological disorders (e.g. asthma, acquired immunodeficient syndrome
 CC (AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease,
 CC sepsis, acne, psoriasis and lupus erythematosus), neural system
 CC disorders, respiratory disorders, olfactory disorders and wound
 CC healing. The present sequence represents an NHP of the invention the
 CC gene for which is located on the X chromosome.
 XX
 SQ Sequence 711 AA;
 Query Match 88.0%; Score 3775; DB 22; Length 711;
 Best Local Similarity 99.3%; Pred. No. 1.5e-311;
 Matches 704; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 62 MNAGDKWSAFLEKQSTLAQWYPLQETQNTLVKQLQALQONGSSVLSKSKRLNTILN 121
 DB 1 MNAGDKWSAFLEKQSTLAQWYPLQETQNTLVKQLQALQONGSSVLSKSKRLNTILN 60
 QY 122 TMSTIYSTGKVCNPNPQBCLLLEPGLNETMANSNDYNERLWAWSRSEVGKQLRPLYE 181
 DB 61 TMSTIYSTGKVCNPNPQBCLLLEPGLNETMANSNDYNERLWAWSRSEVGKQLRPLYE 120
 QY 182 EYVVLKEMARANHVEDYGDYWRGDIYVNGVDYDYSRGQIIEDEHTPEERIKPLYEHLH 241
 DB 121 EYVVLKEMARANHVEDYGDYWRGDIYVNGVDYDYSRGQIIEDEHTPEERIKPLYEHLH 180
 QY 242 AYVPAKLMNAVPSYISPIGCLPAHLIGDMWGRFTWNLVSLTVPFQOKENIDVTAMVQA 301
 DB 181 AYVPAKLMNAVPSYISPIGCLPAHLIGDMWGRFTWNLVSLTVPFQOKENIDVTAMVQA 240
 QY 302 WDAQRIKFAEKFPFVSVGLPNTQGFWNSMLTDPGNQKAVCHPTAWDLKGDPRILMC 361
 DB 241 WDAQRIKFAEKFPFVSVGLPNTQGFWNSMLTDPGNQKAVCHPTAWDLKGDPRILMC 300
 QY 362 TKVTWDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGRTMSLSAATPKHLKSI 421
 DB 301 TKVTWDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGRTMSLSAATPKHLKSI 360
 QY 422 GLLSPDFQEDNETEINFLKQALTIYGLTPFTYMLEKRWMMVFKEIPKQOMKQWEMK 481
 DB 361 GLLSPDFQEDNETEINFLKQALTIYGLTPFTYMLEKRWMMVFKEIPKQOMKQWEMK 420
 QY 482 REIVGVVEPVPHDETCDPASLPHVNDYSFRYYRTLYQFOFQALCOAAKHGGLPKH 541
 DB 421 REIVGVVEPVPHDETCDPASLPHVNDYSFRYYRTLYQFOFQALCOAAKHGGLPKH 480
 QY 542 CDSNSTEAGOKLPNMLRGLKSEFWTLALENVVGAQNMNVRPLLNYFPELFTWLKQKN 601
 DB 481 CDSNSTEAGOKLPNMLRGLKSEFWTLALENVVGAQNMNVRPLLNYFPELFTWLKQKN 540
 QY 602 SFVGSWTDWSPYADQSIKVRISLKSALGDKAVENDNEMYLFRSSVAVAMROYFLKVKNQ 661
 DB 541 SFVGSWTDWSPYADQSIKVRISLKSALGDKAVENDNEMYLFRSSVAVAMROYFLKVKNQ 600
 QY 662 MILFGEEDVRVANLKPRISFNFTAPKQVSDIIPTEVEKAIKRSRINDAFRLNDS 721
 DB 601 MILFGEEDVRVANLKPRISFNFTAPKQVSDIIPTEVEKAIKRSRINDAFRLNDS 660
 QY 722 LEFLGIQPTLGPNNQPPVSIWLIVFGVMGVIVGVIVILIFTGIRDRKK 770
 DB 661 LEFLGIQPTLGPNNQPPVSIWLIVFGVMGVIVGVIVILIFTGIRDRKK 709

RESULT 11

AA848097
ID AAB48097 standard; Protein; 805 AA.

XX AC AAB48097;

XX DT 19-MAR-2001 (first entry)

XX DE Mouse Zace2-5 protein.

XX Zace2; metalloenzyme; angiotensin-converting enzyme; ACE; fertility;
KW zinc metalloproteinase; blood pressure; zinc protease; hypertension;
KW ventricular systolic dysfunction; renal impairment; heart failure;
KW scleroderma renal crisis; atherosclerosis; antiinflammatory; mouse;
KW antiarthritic; bradykinin inactivator.

XX OS Mus sp.

XX FH Key Location/Qualifiers

FT Region 19..613
FT /note= "fragment specifically claimed for"
FT Region 19..708
FT /note= "fragment specifically claimed for"
FT Region 19..738
FT /note= "fragment specifically claimed for"
FT Region 19..805
FT /note= "fragment specifically claimed for"
FT Region 133..542
FT /note= "fragment specifically claimed for"
FT Region 344..542
FT /note= "fragment specifically claimed for"
FT Region 371..402
FT /note= "fragment specifically claimed for"

XX WO200070032-A1.

XX PD 23-NOV-2000.

XX 03-MAY-2000; 2000WO-US11932.

XX 13-MAY-1999; 99US-0311482.

XX 27-AUG-1999; 99US-0384706.

XX (ZYMO) ZYMOGENETICS INC.

XX Piddington CS, Petrie CR, Shoemaker KE, Bishop PD;

XX WPI; 2001-025018/03.

XX N-PSDB; AAC84368, AAC84369.

XX Angiotensin-converting enzyme, Zace2, useful for treating inflammatory
PT bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases
PT associated with inflammation such as arthritis and enterocolitis -

XX Claim 7; Page 104-109; 125pp; English.

XX The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-
CC converting enzyme is a zinc metalloproteinase that plays roles in blood
CC pressure regulation and fertility. Zace2 can be expressed by standard
CC recombinant methodology. Zace2 polypeptides are useful for treating an
CC inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis),
CC diseases associated with inflammation like arthritis and enterocolitis,
CC as targets for identifying modulators of zinc protease activity, for
CC screening or identifying new angiotensin-converting enzyme (ACE)
CC inhibitors, and as a basis for rational drug design for inhibitory
CC molecules. The nucleic acids can be used to detect the expression of a
CC Zace2 gene in a biological sample, as probes for in vivo diagnosis and
CC for detecting and localizing Zace2 gene expression in tissue samples,
CC to determine whether a subject's chromosomes contain a mutation in the
CC Zace2 gene, and to detect aberrations associated with the Zace2 locus.
XX Inhibitors of ACE are used for treating hypertension of various

CC conditions, including left ventricular systolic dysfunction, progressive
CC renal impairment, scleroderma renal crisis, congestive heart failure due
CC to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be
CC used to treat infertility while Zace2 antagonists are used for inducing
CC infertility. The present sequence represents the mouse Zace2-5 protein.

XX SQ Sequence 805 AA;

Query Match 83.4%; Score 3579; DB 22; Length 805;

Best Local Similarity 82.1%; Pred. No. 8.3e-295;
Matches 661; Conservative 60; Mismatches 88; Indels 0; Gaps 0;

QY 1 MSSSSMLLSLAVTAQAQSTIEQAKTFLDKFNHAEADLFYQSSLSASNNYNTNTEENVQ 60
DB 1 MSSSSMLLSLAVTAQAQSTIEQAKTFLDKFNHAEADLFYQSSLSASNNYNTNTEENNAQ 60
QY 61 MNMAGDKVSAFLKEQSTLAQVPLQEIQLNVLKQLQALQOQNGSSVLSEKSLNLTIL 120
DB 61 KMSEAAKWSAFYEQSKTAQSFQEIQTPIKQLQALQOQSSSALSADKNQANTIL 120
QY 121 NTWSTIYTGKVCNPNPOECULLLEPGLNEIMANSIDYNERLWAWESVRSEVQKLRPLY 180
DB 121 NTWSTIYTGKVCNPNPOECULLLEPGLNEIMANSIDYNERLWAWESVRSEVQKLRPLY 180
QY 181 EBYVVLKQEMARAHYEDYDGYWRGDYEVNGVDYDYSRGOLIEDVETFEIPLVEHL 240
DB 181 EBYVVLKQEMARAHYEDYDGYWRGDYEVNGVDYDYSRGOLIEDVETFEIPLVEHL 240
QY 241 HAYVRKLNAYPSYISPIGCLPAHLGDMWRFTNLYSLTPGQKNDIVTDAMVQ 300
DB 241 HAYVRKLNAYPSYISPIGCLPAHLGDMWRFTNLYSLTPGQKNDIVTDAMVQ 300
QY 301 AWAQRIKFAEAKFFSVSVGLPNMTQGFWNSMLTDPGNVQKAVCHTAMDLGKDFRILM 360
DB 301 GWAERIFQAEAKFFSVSVGLPHMTQGFWNSMLTDPGNVQKAVCHTAMDLGKDFRILM 360
QY 361 CTKYTMDDDLTAHHENGHIQYDMAYAAOPFLRNAGNEGFHEAVGEINSLSAATPKHLKS 420
DB 361 CTKYTMDDDLTAHHENGHIQYDMAYAAOPFLRNAGNEGFHEAVGEINSLSAATPKHLKS 420
QY 421 IGLLSEDFQEDNETEINFLKQALITVGLPTMYLKWMMVFKGEIPKQMMKKWEM 480
DB 421 IGLLSEDFQEDNETEINFLKQALITVGLPTMYLKWMMVFKGEIPKQMMKKWEM 480
QY 481 KRETVGVVPEPHDETCDPASLPHVSNDSYRIRYVYTRTYQFOQALCOAKHGLSLH 540
DB 481 KRETVGVVPEPHDETCDPASLPHVSNDSYRIRYVYTRTYQFOQALCOAKHGLSLH 540
QY 541 KCDISNSTEAGQKLFNMLRGKSEPTLALENVGAKNNVRPLNLYPEPLFTMLKDNK 600
DB 541 KCDISNSTEAGQKLFNMLRGKSEPTLALENVGAKNNVRPLNLYPEPLFTMLKDNK 600
QY 601 NSFVGMSTDSVPADQSIKVRISLKSALGDKAYEWNDEMVLFRSSVAYAMKQYFLKVK 660
DB 601 NSFVGMSTDSVPADQSIKVRISLKSALGDKAYEWNDEMVLFRSSVAYAMKQYFLKVK 660
QY 661 QMILFGEEDVRVANLKRISFNFFVTAPKNVSDIIPRTEVEKAIMRSRINDAFRLNDN 720
DB 661 QMILFGEEDVRVANLKRISFNFFVTAPKNVSDIIPRTEVEKAIMRSRINDAFRLNDN 720
QY 721 SLRFLGIQPTLGPFPNPPVSIIMLVGVVMGVIVGVIVILITGIRDRKKKKKARSGNP 780
DB 721 SLRFLGIQPTLGPFPNPPVSIIMLVGVVMGVIVGVIVILITGIRDRKKKKKARSGNP 780
QY 781 YASIDTSKGNNGPQNTDDVQTSF 805
DB 781 YASIDTSKGNNGPQNTDDVQTSF 805

RESULT 12

ASU07733

ID ABU07733 standard; Protein; 805 AA.

XX

ABU07733;
 27-MAY-2003 (first entry)
 Mouse zinc metalloproteinase mZace-5.
 Mouse; enzyme; mZace-5; zinc metalloproteinase; ulcerative colitis;
 inflammation; inflammatory bowel disease; arthritis; enterocolitis;
 Crohn's disease; gene therapy; transgenic.
 Mus sp.
 US2002177211-A1.
 28-NOV-2002.
 16-OCT-2001; 2001US-0978385.
 13-MAY-1999; 99US-133952P.
 27-AUG-1999; 99US-151181P.
 03-MAY-2000; 2000US-0563516.
 (ZYMO) ZYMOGENETICS INC.
 Piddington CS, Petrie C, Shoemaker KE, Bishop PD;
 WPI; 2003-328489/31.
 N-PSDB; ABX93335.
 Isolated human or murine Zace2 polypeptide useful for reducing
 inflammation in conditions such as inflammatory bowel disease,
 arthritis, enterocolitis, ulcerative colitis and Crohn's disease -
 Claim 1; Page 46-48; 57pp; English.
 The invention relates to an isolated polypeptide, comprising fully
 defined human Zace2, murine Zace-5, or murine Zace2-10 polypeptide. An
 expression vector containing Zace2 polynucleotide is useful for producing
 Zace2 protein. The polynucleotide is useful as a diagnostic probe for
 detecting a product of Zace2 gene expression in a biological sample. The
 polypeptide is also useful for decreasing inflammation associated with a
 condition such as inflammatory bowel disease, arthritis or enterocolitis.
 The polypeptide is also useful for treating Crohn's disease and
 ulcerative colitis. The polypeptide is useful for producing labelled
 angiotensin II, for identifying modulators of zinc protease activity and
 for identifying angiotensin converting enzyme (ACE) inhibitors. The
 polynucleotide is useful in gene therapy techniques to treat the above
 mentioned disorders. The polynucleotide is also useful for determining
 whether a subject's chromosome contains a mutation in the Zace2 gene. The
 present sequence represents the amino acid sequence of mouse zinc
 metalloproteinase mZace-5.
 Sequence 805 AA;
 Query Match 83.4%; Score 3579; DB 24; Length 805;
 Best Local Similarity 82.1%; Pred. No. 8.3e-295;
 Matches 561; Conservative 60; Mismatches 84; Indels 0; Gaps 0;
 1 MSSSSWLLSLVAVTAQSTIEQAKTFLDKFNHEADLFYQSSLASWNNYNITEENVQ 60
 1 MSSSSWLLSLVAVTAQSTIEQAKTFLDKFNHEADLFYQSSLASWNNYNITEENVQ 60
 61 MNNAAGDWSAFLEQSTLAQMYPLQIQLNLTQALQALQNGSSVLSDEKSKRLNITL 120
 61 KMSEAAKWSAFYBEQSKTAQSPSLQIQTPIIKRQLQALQSSGALSADNKKQLNITL 120
 121 NTMSTIYTGKVCNPDNPQECCLLEPGNLEIMANSIDYNERLWAWESWSEVKGQRLPY 180
 121 NTMSTIYTGKVCNPKNPQECCLLEPGLEIMATSTDYNSRLWAWEGWAEVKGQRLPY 180
 181 EBYVVLKNEARAHYEDYGVWGYEVNGVDGYDSRGQLTJEDVEHTFEIKPLYEHL 240
 181 EBYVVLKNEARANNYNDYGVWGYEAGDGYNNRNQLIEDYVTFBIKPLYEHL 240

QY 241 HAYVRAKLMNAYPSYISPIGCLPAHLIGDMKMGFWNTNLYSLVTFPQCKKNIDVTDAMWQ 300
 DB 241 HAYVRAKLMNAYPSYISPIGCLPAHLIGDMKMGFWNTNLYSLVTFPQCKKNIDVTDAMWQ 300
 QY 301 AWDAQRIKAEAEKFFSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAMDLGKGDFRIAM 360
 DB 301 GWDARIKAEAEKFFSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAMDLGKGDFRIAM 360
 QY 361 CTXVTMDLFTAHHEMGHIQYDMAYAAQPELLNGEGFHEAVGEIMSLSATPKHLKS 420
 DB 361 CTXVTMDLFTAHHEMGHIQYDMAYAAQPELLNGEGFHEAVGEIMSLSATPKHLKS 420
 QY 421 IGLSPDFQEDNTEINFLKQALTIYGTLPFTYMLEKRWMMVFKGEIPKQOMKQWEM 480
 DB 421 IGLSPDFQEDNTEINFLKQALTIYGTLPFTYMLEKRWMMVFKGEIPKQOMKQWEM 480
 QY 481 KREIVGVVEPVPDHTCYCPASLPHVSNDSFYRYTTRTYQFOFQALCOAAKHGPHL 540
 DB 481 KREIVGVVEPVPDHTCYCPASLPHVSNDSFYRYTTRTYQFOFQALCOAAKHGPHL 540
 QY 541 KCDISNTEAGQKLFNMLRGKSEPTWALLENVVGAKMMVRELLNYFPPLFTWLKQNK 600
 DB 541 KCDISNTEAGQKLFNMLRGKSEPTWALLENVVGAKMMVRELLNYFPPLFTWLKQNK 600
 QY 601 NSFVGMSTWSPYADQSIKVRISLKSALGDKAYEMNDNEMFLPRSSVAYAMROYFLKVN 660
 DB 601 NSFVGMSTWSPYADQSIKVRISLKSALGDKAYEMNDNEMFLPRSSVAYAMROYFLKVN 660
 QY 661 QMILFGEEDVRVANLKRISFNFTVAPKNVSDIIPTEVEKAIKMSRSHINDAFRLND 720
 DB 661 QMILFGEEDVRVANLKRISFNFTVAPKNVSDIIPTEVEKAIKMSRSHINDAFRLND 720
 QY 721 SLEFLGIQTLTLPNPPVPSIWLIVFGVMGVIVGVIVILIFTGIRDRKKKKKARGENP 780
 DB 721 SLEFLGIQTLTLPNPPVPSIWLIVFGVMGVIVGVIVILIFTGIRDRKKKKKARGENP 780
 QY 781 YASIDISKGNPPQFQNTDVTQSF 805
 DB 781 YASIDISKGNPPQFQNTDVTQSF 805
 RESULT 13
 AAB48098
 ID AAB48098 standard; Protein; 805 AA.
 AC AAB48098;
 DT 19-MAR-2001 (first entry)
 DE Mouse Zace2-10 protein.
 KW Zace2; metalloenzyme; angiotensin-converting enzyme; ACE; fertility;
 zinc metalloproteinase; blood pressure; zinc protease; hypertension;
 ventricular systolic dysfunction; renal impairment; heart failure;
 scleroderma renal crisis; atherosclerosis; antiinflammatory; mouse;
 antiarthritic; bradykinin inactivator.
 Mus sp.
 Key Location/Qualifiers
 Region 19..613
 /note= "fragment specifically claimed for"
 Region 19..708
 /note= "fragment specifically claimed for"
 Region 19..738
 /note= "fragment specifically claimed for"
 Region 19..805
 /note= "fragment specifically claimed for"
 Region 133..542
 /note= "fragment specifically claimed for"
 Region 344..542
 /note= "fragment specifically claimed for"

PT Region 371..402
 XX /note= "fragment specifically claimed for"
 PN WO200070032-A1.
 XX 23-NOV-2000.
 XX 03-MAY-2000; 2000WO-US11932.
 XX 13-MAY-1999; 99US-0311482.
 XX 27-AUG-1999; 99US-0384706.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Piddington CS, Petrie CR, Shoemaker KE, Bishop PD;
 XX WPI; 2001-025018/03.
 XX N-PSDB; AAC84370.
 XX Angiotensin-converting enzyme, Zace2, useful for treating inflammatory
 PT bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases
 PT associated with inflammation such as arthritis and enterocolitis -
 XX
 PS Claim 7; Page 113-118; 125pp; English.
 XX
 CC The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-
 CC converting enzyme is a zinc metallopeptidase that plays roles in blood
 CC pressure regulation and fertility. Zace2 can be expressed by standard
 CC recombinant methodology. Zace2 polypeptides are useful for treating an
 CC inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis),
 CC diseases associated with inflammation like arthritis and enterocolitis,
 CC as targets for identifying modulators of zinc protease activity, for
 CC screening or identifying new angiotensin-converting enzyme (ACE)
 CC inhibitors, and as a basis for rational drug design for inhibitory
 CC molecules. The nucleic acids can be used to detect the expression of a
 CC Zace2 gene in a biological sample, as probes for in vivo diagnosis and
 CC for detecting and localizing Zace2 gene expression in tissue samples,
 CC to determine whether a subject's chromosomes contain a mutation in the
 CC Zace2 gene, and to detect aberrations associated with the Zace2 locus.
 CC Inhibitors of ACE are used for treating hypertension of various
 CC conditions, including left ventricular systolic dysfunction, progressive
 CC renal impairment, scleroderma renal crisis, congestive heart failure due
 CC to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be
 CC used to treat infertility while Zace2 antagonists are used for inducing
 CC infertility. The present sequence represents the mouse Zace2-10 protein.
 XX
 XX Sequence 805 AA;
 SQ
 Query Match 83.0%; Score 3561; DB 22; Length 805;
 Best Local Similarity 81.9%; Pred. No. 2.8e-293;
 Matches 659; Conservative 60; Mismatches 86; Indels 0; Gaps 0;
 QY 1 MSSSSWLLSLVAVTAAGSTIEROAKTFLDKFNHEADLFVQSSLASWNTNTNTEENQ 60
 DB 1 MSSSSWLLSLVAVTAAGSTIEROAKTFLDKFNHEADLFVQSSLASWNTNTNTEENQ 60
 QY 61 NNNAGDKWSAPLKEQSTLAQYPIQETQNTLVKQLQALQOQSSVLSDEKSKRINTIL 120
 DB 61 KMSEAAKWSAFYERQSQTAQSFSLQEIQTPIIKRQLQALQOQSSALSADKNKQNTIL 120
 QY 121 NTWSTIYTGKVCNPDNPQECILLEGNETMANSLDYNEELMAWESWRSEVCKQLRPLY 180
 DB 121 NTWSTIYTGKVCNPDNPQECILLEGNETMANSLDYNEELMAWESWRSEVCKQLRPLY 180
 QY 181 EYVVLKNEMARANYHYDGYWRGDYEVNGVDYVSRGQLTEDVEHTEETFKPIYEHL 240
 DB 181 EYVVLKNEMARANNYNDYDGYWRGDYEAEGADGYNRYNRQLIEDVERTFAEIKPIYEHL 240
 QY 241 HAYVRKLMNAYPSYISPIGCLPAHLGDMWGRFTWNLISLTVPFGOKPNIIDVTDAWQ 300
 DB 241 HAYVRKLMNTYPSYISPIGCLPAHLGDMWGRFTWNLISLTVPFGOKPNIIDVTDAWQ 300
 QY 301 AWDQRIFKEAEKFFVSVGLPNTQGFWNSMLTDPGNVQKAVCHPTAWDLGKGDFFILM 360

DB 301 GWDARLIFQAEKFFVSVGLPNTQGFWNSMLTDPADGRKVCHPTAWDLGKGDFFILM 360
 QY 361 CTKVTWDDILTAAHENGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
 DB 361 CTKVTWDDILTAAHENGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
 QY 421 IGLSPDFQEDNTEINFLLKQALTIVGTLPTTYMLEKRWNVFKGEIPKQOMKKWHEM 480
 DB 421 IGLSPDFQEDNTEINFLLKQALTIVGTLPTTYMLEKRWNVFKGEIPKQOMKKWHEM 480
 QY 481 KREIVGVPEVPHDETYCDPASLHVSNDSYFIRYVTRTLQFOFOEALCOAAKHEGPLH 540
 DB 481 KREIVGVPEVPHDETYCDPASLHVSNDSYFIRYVTRTLQFOFOEALCOAAKHEGPLH 540
 QY 541 KCDISNSTEAGOKLFNMLELKGSEBWTLELVGAKNNVRPLNLYPEPLFTWLDQNK 600
 DB 541 KCDISNSTEAGOKLFNMLELKGSEBWTLELVGAKNNVRPLNLYPEPLFTWLDQNK 600
 QY 601 NSFVGNSTWSPVADOSIKVRISLSKALGDKAYENDNEMYLFRSSVAYAMROYFLKVK 660
 DB 601 NSFVGNSTWSPVADOSIKVRISLSKALGDKAYENDNEMYLFRSSVAYAMROYFLKVK 660
 QY 661 QMLFGEEDVVRVANLKRISFNFFVTAPKQVSDIIPRTEVEKAIMRSRINDAPRLND 720
 DB 661 QMLFGEEDVVRVANLKRISFNFFVTAPKQVSDIIPRTEVEKAIMRSRINDAPRLND 720
 QY 721 SLFLGIQPTLGPNOPPVSIWLVGVGVGVVIVGIVLITFTGIRDRKKKKARSGENP 780
 DB 721 SLFLGIQPTLGPNOPPVSIWLVGVGVGVVIVGIVLITFTGIRDRKKKKARSGENP 780
 QY 781 YASIDISKGNENFGONTDDVQTSF 805
 DB 781 YDSMDICKGESNAGFQNSDDACTSF 805
 RESULT 14
 ABU07734
 ID ABU07734 standard; Protein; 805 AA.
 AC ABU07734;
 XX 27-MAY-2003 (first entry)
 DT Mouse zinc metallopeptidase mZace-10.
 DE Mouse
 KW Mouse; enzyme; mZace-10; zinc metallopeptidase; ulcerative colitis;
 KW inflammation; inflammatory bowel disease; arthritis; enterocolitis;
 XX Crohn's disease; gene therapy; transgenic
 OS Mus sp.
 XX US2002177211-A1.
 XX 28-NOV-2002.
 XX 16-OCT-2001; 2001US-0978385.
 XX 13-MAY-1999; 99US-133952P.
 PR 27-AUG-1999; 99US-151181P.
 PR 03-MAY-2000; 2000US-0563516.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Piddington CS, Petrie C, Shoemaker KE, Bishop PD;
 XX WPI; 2003-328489/31.
 DR N-PSDB; ABX93337.
 XX Isolated human or murine Zace2 polypeptide useful for reducing
 PT inflammation in conditions such as inflammatory bowel disease,
 PT arthritis, enterocolitis, ulcerative colitis and Crohn's disease -
 XX

PS Claim 1; Page 52-54; 57pp; English.

CC The invention relates to an isolated polypeptide, comprising fully
 CC defined human Zace2, murine Zace-5, or murine Zace2-10 polypeptide. An
 CC expression vector containing Zace2 polynucleotide is useful for producing
 CC Zace2 protein. The polynucleotide is useful as a diagnostic probe for
 CC detecting a product of Zace2 gene expression in a biological sample. The
 CC polypeptide is also useful for decreasing inflammation associated with a
 CC condition such as inflammatory bowel disease, arthritis or enterocolitis.
 CC The polypeptide is also useful for treating Crohn's disease and
 CC ulcerative colitis. The polypeptide is useful for producing labelled
 CC angiotensin II, for identifying modulators of zinc protease activity and
 CC for identifying angiotensin converting enzyme (ACE) inhibitors. The
 CC polynucleotide is useful in gene therapy techniques to treat the above
 CC mentioned disorders. The polynucleotide is also useful for determining
 CC whether a subject's chromosome contains a mutation in the Zace2 gene. The
 CC present sequence represents the amino acid sequence of mouse zinc
 CC metalloproteinase mZace-10.

XX SQ Sequence 805 AA;

Query Match 83.08; Score 3561; DB 24; Length 805;

Best Local Similarity 81.99; Pred. No. 2.8e-293;
 Matches 659; Conservative 60; Mismatches 86; Indels 0; Gaps 0;

QY 1 MSSSSWLLLSVAVTAQAQSTIEQAKTFLDKFNHEADLFYQSSLSASWNYNTNTEENVQ 60
 RP 1 MSSSSWLLLSVAVTAQAQSTIEQAKTFLDKFNHEADLFYQSSLSASWNYNTNTEENVQ 60
 QY 61 NNNNAGDKWSAFLEKQSTLAQMPLOEIQNTLVKQLQALQNGSSVLSEDKSKRLNTIL 120
 DB 61 KMSAAAKWSAFYEQKTAQSPSLQEIQTPIKRLQALQNGSSALSADKNQLNTIL 120
 QY 121 NTMTTISTGKVNPNQPCLLLEPGLNEMANSLDYNERLWAVESWRSEVQKQRLPLY 180
 DB 121 NTMTTISTGKVNPNQPCLLLEPGLNEMANSLDYNERLWAVESWRSEVQKQRLPLY 180
 QY 181 BEYVVLKNEMARAHYEDYDYGWDYGVNGVDYSGQLIEDVHTPEIKPLVEHL 240
 DB 181 BEYVVLKNEMARAHYEDYDYGWDYGVNGVDYSGQLIEDVHTPEIKPLVEHL 240
 QY 241 HAYVRKLMNAPYSYIPICPLPAHLGDMWGFNTNLSLTPFGQKPNIDVTDMNQ 300
 DB 241 HAYVRKLMNAPYSYIPICPLPAHLGDMWGFNTNLSLTPFGQKPNIDVTDMNQ 300
 QY 301 AWDARIFKEAEKFFSVGLPNMTQGFWNSMLTDPNVOKAVCHPTAWDLGKGFILM 360
 DB 301 AWDARIFKEAEKFFSVGLPNMTQGFWNSMLTDPNVOKAVCHPTAWDLGKGFILM 360
 QY 361 CTKVTMDDFLTAHEMGHIQYDMAYAAQPELLNGANEGFHEAVGEIMSLSAATPKHLKS 420
 DB 361 CTKVTMDDFLTAHEMGHIQYDMAYAAQPELLNGANEGFHEAVGEIMSLSAATPKHLKS 420
 QY 421 IGLSPQFQENETINFLIKQALITVGLTPFTYMLEKRWNVFGEIPKQWKKWEM 480
 DB 421 IGLSPQFQENETINFLIKQALITVGLTPFTYMLEKRWNVFGEIPKQWKKWEM 480
 QY 481 KREIVGVVEPVPFHDTECDPASLFHVSNDYSFIRYTRTYTRTYTRTYTRTYTRTYTRTY 540
 DB 481 KREIVGVVEPVPFHDTECDPASLFHVSNDYSFIRYTRTYTRTYTRTYTRTYTRTYTRTY 540
 QY 541 KCDISNSTEAGOKLFWMLRGKSEPMTLAENNVGKANNVRLNYPFLTKDQNK 600
 DB 541 KCDISNSTEAGOKLFWMLRGKSEPMTLAENNVGKANNVRLNYPFLTKDQNK 600
 QY 601 NSFVGNSTWSPYADQSIKIVRISLKSALGDKAYEMNDNEMYLFRSSVAYAMRQYFLKVN 660
 DB 601 NSFVGNSTWSPYADQSIKIVRISLKSALGDKAYEMNDNEMYLFRSSVAYAMRQYFLKVN 660
 QY 661 QMILFGEDVAVALKRIFGNFVTPAKVNSDIIIPRTVEKAIKMSRSRINDAFRLNDN 720
 DB 661 QMILFGEDVAVALKRIFGNFVTPAKVNSDIIIPRTVEKAIKMSRSRINDAFRLNDN 720

QY 721 SLEFLGIQPTLGPBNOPPPYSIMLIVFGVGMVIVGIVLIFTGIRDEKKKNSGSENP 780
 DB 721 SLEFLGIQPTLGPBNOPPPYSIMLIVFGVGMVIVGIVLIFTGIRDEKKKNSGSENP 780
 QY 781 YASIDISKGNENPGFQNTDDVQTSF 805
 DB 781 YDSMDIGKGSNAGFQNSDDAQTFSF 805
 RESULT 15
 AAU12207
 ID AAU12207 standard; Protein; 555 AA.
 XX AC AAU12207;
 XX DT 24-OCT-2001 (first entry)
 XX DE Human PRO1885 polypeptide sequence.
 XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy.
 XX OS Homo sapiens.
 XX PN WO200140466-A2.
 XX PD 07-JUN-2001.
 XX PF 01-DEC-2000; 2000WO-US32678.
 XX PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 09-DEC-1999; 99US-0170262.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31243.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.
 (GETH) GENENTECH INC.
 PA Baker KP, Beresini M, Deforge L, Desnoyers L, Pilvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PU, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 DR WPI; 2001-408281/43.
 DR N-PSDB; AAS21279.
 XX Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical

XX

PS Claim 12; Fig 72; 813pp; English.

XX

AAU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor- α (TNF- α) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.

XX SQ Sequence 555 AA;

Query Match 69.4%; Score 2979; DB 22; Length 555;

Best Local Similarity 99.8%; Pred. No. 4.5e-244;

Matches 553; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSSSWLLLSLVAVTAAGSTIEBQAKTFLDKFNHEAEDLFYQSSLSASWNTNTITEENVQ 60

Db 1 MSSSSWLLLSLVAVTAAGSTIEBQAKTFLDKFNHEAEDLFYQSSLSASWNTNTITEENVQ 60

QY 61 NNNAAGDKWSAFLEQSTLAQMPLOEQNTLVKLQALQONGSSVLSEDSKRLNTIL 120

Db 61 NNNAAGDKWSAFLEQSTLAQMPLOEQNTLVKLQALQONGSSVLSEDSKRLNTIL 120

QY 121 NTWSTIYSGKVCNPDNFECLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLY 180

Qb 121 NTWSTIYSGKVCNPDNFECLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLY 180

QY 181 EYVVLKNEMARANHYEDYDWRGDYEVNGDYGYSRGQLIEDVHTFEEIKPLYEHL 240

Db 181 EYVVLKNEMARANHYEDYDWRGDYEVNGDYGYSRGQLIEDVHTFEEIKPLYEHL 240

QY 241 HAYVRAKLNAYPSYISPIGCLPAHLGDMWGRFWTNLYSLTVFFGQKPNIDVTDAMVDQ 300

Db 241 HAYVRAKLNAYPSYISPIGCLPAHLGDMWGRFWTNLYSLTVFFGQKPNIDVTDAMVDQ 300

QY 301 ANDAQRIFKEAEKFFVSVGLNMTQGFWENSMITDGNVQKAVCHPTANDLGKDFRILM 360

Db 301 ANDAQRIFKEAEKFFVSVGLNMTQGFWENSMITDGNVQKAVCHPTANDLGKDFRILM 360

QY 361 CTXVTMDDFLTAHHEMGHIQYDMAAQAQFFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420

Db 361 CTXVTMDDFLTAHHEMGHIQYDMAAQAQFFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420

QY 421 IGLSPDFQEDNETEINLLKQALTVIGTLPTVYMLKRWMMVKGEIPKQDQWKKWEM 480

Db 421 IGLSPDFQEDNETEINLLKQALTVIGTLPTVYMLKRWMMVKGEIPKQDQWKKWEM 480

QY 481 KREIVGVVEFVPHDETYCDPASLFHVSNDYSFIRYTRTLYQFQFQALCOAAKHEGPLH 540

Db 481 KREIVGVVEFVPHDETYCDPASLFHVSNDYSFIRYTRTLYQFQFQALCOAAKHEGPLH 540

QY 541 KCDISNSTEAGQKL 554

Db 541 KCDISNSTEAGQKL 554

Search completed: February 19, 2004, 19:49:43

Job time : 50 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 19, 2004, 19:48:48 ; Search time 21 Seconds
(without alignments)
1621.916 Million cell updates/sec

Title: US-09-163-648-2
Perfect score: 4291
Sequence: 1 MSSSSWLLSLVAVTAAQST.....LSKGNPGRQNTDVTGTSF 805

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/aa/5B COMB.pcp:*
3: /cgn2_6/prodata/1/aa/6A COMB.pcp:*
4: /cgn2_6/prodata/1/aa/6B COMB.pcp:*
5: /cgn2_6/prodata/1/aa/6C COMB.pcp:*
6: /cgn2_6/prodata/1/aa/6D COMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4291	100.0	805	3	US-08-989-299-2
2	1344	31.3	732	1	US-08-481-626-2
3	1344	31.3	732	3	US-08-989-299-4
4	1337	31.2	1306	3	US-08-989-299-7
5	1334	31.1	732	3	US-08-989-299-5
6	1334	31.1	1312	3	US-08-989-299-8
7	1310	30.5	1313	3	US-08-989-299-9
8	1283	29.9	1310	3	US-08-989-299-10
9	1283	29.9	737	3	US-08-989-299-6
10	1090	25.4	615	3	US-08-989-299-11
11	990	23.1	694	3	US-09-440-325A-1
12	990	23.1	694	4	US-09-846-996A-1
13	642.5	15.0	907	3	US-08-989-299-12
14	376	8.8	212	4	US-09-996-243-387
15	131	3.1	615	4	US-09-107-532A-6507
16	124	2.9	990	2	US-08-645-192B-35
17	120	2.8	990	2	US-08-392-625-20
18	120	2.8	990	2	US-08-466-961A-20
19	118	2.7	3878	4	US-09-914-259-11
20	116.5	2.7	683	3	US-08-630-916A-46
21	115.5	2.7	2008	4	US-09-091-501B-8
22	115.5	2.7	3433	4	US-09-091-501B-10
23	113.5	2.6	665	3	US-08-844-059-2
24	113.5	2.6	665	3	US-09-431-202-2
25	109.5	2.5	499	4	US-09-107-532A-5524
26	109	2.5	686	4	US-09-328-352-4503
27	104	2.4	834	1	US-08-491-357-2

26	104	2.4	834	3	US-08-968-633-2	Sequence 2, Appli
29	104	2.4	834	3	US-09-195-466-2	Sequence 2, Appli
30	104	2.4	834	5	PCT-US96-10823-2	Sequence 2, Appli
31	102.5	2.4	429	4	US-09-194-468A-45	Sequence 45, Appli
32	102.5	2.4	631	3	US-08-448-489-17	Sequence 17, Appli
33	102.5	2.4	660	3	US-08-704-711A-18	Sequence 18, Appli
34	102.5	2.4	660	4	US-09-521-220-18	Sequence 18, Appli
35	102.5	2.4	660	4	US-09-391-104-19	Sequence 19, Appli
36	102	2.4	3169	4	US-09-453-702B-257	Sequence 257, App
37	101.5	2.4	450	3	US-09-306-593-13	Sequence 13, Appli
38	101.5	2.4	560	4	US-09-134-001C-3153	Sequence 3153, Ap
39	101	2.4	984	4	US-09-328-352-6926	Sequence 6926, Ap
40	101	2.4	998	4	US-09-198-452A-841	Sequence 841, App
41	100	2.3	674	4	US-09-107-532A-6201	Sequence 6201, Ap
42	99.5	2.3	789	4	US-09-002-285-84	Sequence 84, Appli
43	99.5	2.3	789	4	US-09-589-477-84	Sequence 84, Appli
44	99.5	2.3	930	4	US-08-953-040-2	Sequence 2, Appli
45	99	2.3	800	4	US-09-107-532A-4095	Sequence 4095, Ap

ALIGNMENTS

RESULT 1
US-08-989-299-2
; Sequence 2, Application US/08989299
; Patent No. 6194556
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,299
; FILING DATE: 11-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold E. Beth
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-025.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 805 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-989-299-2

Query Match 100.0%; Score 4291; DB 3; Length 805;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSSSWLLSLVAVTAAQSTIEQAKTFLDKFNHEADLFYQSSLSASNNYNTNITENVQ 60
Db 1 MSSSSWLLSLVAVTAAQSTIEQAKTFLDKFNHEADLFYQSSLSASNNYNTNITENVQ 60
QY 61 NNNRAGDKWSAFLEKQSTLAQMPLEQNTLVKLQALQNGSSVLSEDKSRRLATIL 120

Db 61 NNNAGDKWSAFLEKEQSTLQMYPLQEIQLTQVLQLOALQNGSSVSEKSKRLNTIL 120
QY 121 NTMTSTYTGKVCNPNPQECCLLEPGLNEIMANSLDYNRLWAWESWRSEVQKRLPLY 180
Db 121 NTMTSTYTGKVCNPNPQECCLLEPGLNEIMANSLDYNRLWAWESWRSEVQKRLPLY 180
QY 181 EYVVLKNEMARANHYEDYGYWKGDEYVNGVDGYDYSRGQLIEDVEHTFEIKPLYEHL 240
Db 181 EYVVLKNEMARANHYEDYGYWKGDEYVNGVDGYDYSRGQLIEDVEHTFEIKPLYEHL 240
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Db 301 ANDAQRIIFKEAKKFFSVSVGLPDMTQGWENSMITDGNVQKAVCHPTAWDLGKGBFILM 360
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Db 361 CTKVMTDDFLTAHHEMGHIQYDMAYAAQPELLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
QY 421 IGLLSDFQEDNEETEINFLLKQALTIVGTLPTFTYMLEKRWNVKGEIPKQWKKWEM 480
Db 421 IGLLSDFQEDNEETEINFLLKQALTIVGTLPTFTYMLEKRWNVKGEIPKQWKKWEM 480
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Db 781 YASIDISKGENNPGFQNTDDVQSP 805

RESULT 2
US-08-481-626-2
; Sequence 2, Application US/08481626
; Patent No. 5801040
; GENERAL INFORMATION:
; APPLICANT: Soubrier, Florent
; APPLICANT: Albenc-Gelas, Francois
; APPLICANT: Hubert, Christine
; APPLICANT: Corvel, Pierre
; TITLE OF INVENTION: Nucleic Acid Coding for the Human
; TITLE OF INVENTION: Nucleic Acid Coding for the Human
; TITLE OF INVENTION: Uses, Especially for the In Vitro Screening for this
; TITLE OF INVENTION: Enzyme in the Organism
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,626
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/656,183
FILING DATE: 04-MAR-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 89-09062
FILING DATE: 05-JUL-1989
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 04958-0006-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 732 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-481-626-2

Query Match 31.3%; Score 1344; DB 1; Length 732;
Best Local Similarity 41.8%; Pred. No. 7,1e-120; Mismatches 204; Indels 38; Gaps 10;
Matches 259; Conservative 119; Mismatches 204; Indels 38; Gaps 10;

QY 15 TAAQS-----TIEQAKTFLDKENHEADLFYQSSLASWNTNTITB-----NVQNM 62
Db 61 TSAQSNLITDSEAKSFVEYDRTSQVWNEYAEANWNTNTITTSKILQKNQIA 120
QY 63 NNAQDKWSAFLEKEQSTLQMYPLQEIQLTQVLQLOALQNGSSVSEKSKRLNTIL 122
Db 121 NHT-----LKYQTQARKFDVNLQNTTIKRIKKVQDLERAAALPAQELEYNKILD 172
QY 123 MSTIYTGKVCNPNPQECCLLEPGLNEIMANSLDYNRLWAWESWRSEVQKRLPLY 182
Db 173 METTYSVATVCHENG--SCLQLEPDLTVNATSKYEDLLWANEGRDKAGRAILOFYFK 230
QY 183 YVVLKNEMARANHYEDYGYWKGDEYVNGVDGYDYSRGQLIEDVEHTFEIKPLYEHL 242
Db 231 YVELINQAAARLNGYVDAGDSWRSMTYTPSLE-----QDLERLFOELQVLYNLHA 280
QY 243 YVRAKLMNAY-PSYISPIGCLPAHLGDMWGFNTLYSLTVPGQKNGENIDVTAMVDQ 301
Db 281 YVRAKLMNAY-PSYISPIGCLPAHLGDMWGFNTLYSLTVPGQKNGENIDVTAMVDQ 340
QY 302 WDAQRIIFKEAKKFFSVSVGLPDMTQGWENSMITDGNVQKAVCHPTAWDLGKGBFILM 360
Db 341 WTPRRMFKEADDFTSLSGLLPVPEFVWKSMLKPTDGRVVCVCHASANDFYNGKDFRIKQ 400
QY 361 CTKVMTDDFLTAHHEMGHIQYDMAYAAQPELLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
Db 401 CTVNLJEDLVVAHHEMGHIQVFMQKOLPVALREGANPGFHEAIGDVLALSSTPKHLHS 460
QY 421 IGLLSDFQEDNEETEINFLLKQALTIVGTLPTFTYMLEKRWNVKGEIPKQWKKWEM 480
Db 461 LNLISSEGGSD-EHDINFLMKALDKIAFPFSLVDQWNRVFDGSIKTENYQSWMSL 519
QY 481 KREIVGVVEPVPHDETCDPASLPHVNDYSFTRYTRTYLQFQCEALCOAAKHEGPLH 540
Db 520 RLKYGQLCPVPRTQGDFFGAKPHIIPSSVPIYRYFVSFIQFQFHEALCOAAKHEGPLH 579
QY 541 KCDISNSTEAGCKLFNMLRKGSEPTLALENVVGAKNVRLNYPPLNPELFTWLKQNK 600

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Db 580 KCDIVQSKAGORLATAMKLGFSRPWPEAMQLITGPNMSASAMLSYFKPLDMLRTENE 639
QY 601 --NSFVGW-STDWSPYADQS 617
Db 640 LHGEKLGWPNQYNWTPNSARS 659

RESULT 3
US-08-989-299-4
; Sequence 4, Application US/08989299
; Patent No. 6194556
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Robinson, Keith E.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: FOLEY, HOAG & ELIOT LLP
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,299
; FILING DATE: 11-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold E., Beth
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-025.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-7000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 732 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-989-299-4

Query Match 31.3%; Score 1344; DB 3; Length 732;
Best Local Similarity 41.8%; Pred. No. 7, 1e-120;
Matches 259; Conservative 119; Mismatches 204; Indels 38; Gaps 10;

QY 15 TAAQS-----TIEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-----NVQNM 62
Db 61 TSAQSNNLVDEAKSVVEYDRTSOVWNEVAEANNNTNITETSKILLQKNMOIA 120
QY 63 NNAQKWSAFLKQSTLAQMYPLQIQLNVLKQLQALQMGSSVLSDKSKRLNTILNT 122
Db 121 NHT-----LKYGTQARKEDVNLQNTTIKRIKKVQDLERAALPAQEELEYNKILLD 172
QY 123 MSTIVSTGVKVPNDPQSCLLLEPLGLNEIMANSLVNERLWAVESVRSEVGKQRLPYEE 182
Db 173 METTIVAVTCHPG--SCLOLEPLDNLNMTATSKYEDLLWAVEGWDKAGRAILOFPYK 230
QY 183 YVVLKNEMARAHYEDYGVYRGVDYGVNGVDYSGQLIEDVHTPEIKPLVEHLHA 242
Db 231 YVELINQAARLNGYVDAGDSWRSMYETPSLE-----QDLERLFOELQFLYINLHA 280
QY 243 YVRAKLMNAY-PSYISPTGCLPAHLGDMGKRWFTNLYSLTVFGQKPIDVDAMDQA 301
Db 281 YVRALHRRHYGAQHNLGSPHALLGNMAQTWSNIYDLVVPFPSPASMDTTEAMLKQG 340
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QY 302 WDAQRIKFAEKFPVSVGLDNMTQGWENSMULTDRGNVQKAVCHPTAMDLCG-DFRILM 360
Db 341 WTPRMFPKADDDFTSLGLLPVPEFNMKSMLEKPTDGRVVVCHASAWDFYNGKDFRIKQ 400
QY 361 CTKVTMDDELTAHEMHGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
Db 401 CTTVNLEDLVVAHEMHGHIQYFMQYKDLFVALREGANPGFHEAIGDVLALSYSTPKHLHS 460
QY 421 IGLLSPDFQEDNETENFLKQALTTVGLPTMYLKKRWVVFKEIPEKQWKKWEM 480
Db 461 LNLISSEGGSD-EHDINFLNKMALDKIAPFSYLDVQKRWVFDGSSITKENYNQEWWSL 519
QY 481 KREIVGVVPEVPHDETYCDPASLFHNSNDYSIRIYTRTLQFQFQFQFQFQFQFQFQFQF 540
Db 520 RLKTYQGLCPVPRTQGDFFGAKFHIPSPVXIRVFSFIQFQFQFQFQFQFQFQFQFQF 579
QY 541 KCDISNSTEAGQKLFNNMLRLGKSEPTLALENVVGAQNNVRLNLYPEPLFTWLKQNK 600
Db 580 KCDIVQSKAGORLATAMKLGFSRPWPEAMQLITGPNMSASAMLSYFKPLDMLRTENE 639
QY 601 --NSFVGW-STDWSPYADQS 617
Db 640 LHGEKLGWPNQYNWTPNSARS 659

RESULT 4
US-08-989-299-7
; Sequence 7, Application US/08989299
; Patent No. 6194556
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Robinson, Keith E.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: FOLEY, HOAG & ELIOT LLP
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,299
; FILING DATE: 11-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold E., Beth
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-025.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1306 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-989-299-7

Query Match 31.2%; Score 1337; DB 3; Length 1306;
Best Local Similarity 41.7%; Pred. No. 8, 8e-119;
Matches 255; Conservative 116; Mismatches 204; Indels 34; Gaps 9;

QY 20 TIEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-----NVQNMNNAQDKWSA 71
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Db 644 TDEAKSFVEEDRTSQVWMEYAEANWNTNITTSKILQKMQIANHT----- 697
Qy 72 FLKEQSTLAQMYFLOBIQNLTKVQLQALQONGSSVLSEDSKRLNTILNTMTSTYSGK 131
Db 698 --LKYGTQARKFVQNLQNTTKRIIKVQDILERAALPAQLEBYNKILLDMETTSVAT 755
Qy 132 VCNPDNFOECLELLEPGLEINMANSLDYNERLWAMESRSVGVKQLRPLYEYVVLKXEMA 191
Db 756 VCHENG--SCLEPDLTNVMTSRKYEDLLWAMEGWEDKAGRAILOFPYKYVELINQAA 813
Qy 192 RANHYEDYGYWGDYEVNGVDGYDSRQQLDEVEHTFEEIKPLYSHLHAYVRAKLMA 251
Db 814 RANGIVDAGOSWRSMTPTSL-----QDLERLFQZQLPYLNLHAYVRAKLHR 863
Qy 252 Y-PSYISPIGCLPAHLGDMGWFNLSYLVFPFGQKPNIDVTDAVVDQAWDAQRIFFE 310
Db 864 YGAQHINLEGIPIAHLGNNWAGTWSNIYDLVVPFSPASMDTTEAMLKQGMTPRMFKE 923
Qy 311 AEKFFVSGLPNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 369
Db 924 ADDFTSLGLLPVPEPFNWSKMLEKFTDGRVVCCHASAWDFYNGKDFRIKQCTVWLEDL 983
Qy 370 LTAHEWHCHTOYMAVAAQFLLRNGANGSFHEAVEIMSLSAATPKHLKSLGLSPDQ 429
Db 984 VRAHEWHCHTOYMAVAAQFLLRNGANGSFHEAVEIMSLSAATPKHLKSLGLSPDQ 1043
Qy 430 EDNTEINFLKQALTTVGLTPFTYMLEKRWNVFKGIPKQDQWKKWMEKREIVGVVE 489
Db 1044 SD-EHDINFLKQALTTVGLTPFTYMLEKRWNVFKGIPKQDQWKKWMEKREIVGVVE 1102
Qy 490 PVPDHTYCDPASLHVSNDYSIRYVTRTYQFQFALCOAAGHGLKCDISNSTE 549
Db 1103 PVPRTQGDGPAKFIHPSVVPVIRYVFSFIQFQFALCOAAGHGLKCDISNSTE 1162
Qy 550 AGOKLPMRLKGEKPEKTLAENVGAKNNVRPLNYPELFTWLDKQNK--NSFVGM- 606
Db 1163 AGOKLPMRLKGEKPEKTLAENVGAKNNVRPLNYPELFTWLDKQNK--NSFVGM- 1222
Qy 607 STDMSPYADQS 617
Db 1223 QYNWTPNSARS 1233

RESULT 5
US-08-989-299-5
; Sequence 5, Application US/08989299
; Patent No. 6194556
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,299
; FILING DATE: 11-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold E. Beth
; REGISTRATION NUMBER: 35,430
```

```
REFERENCE/DOCKET NUMBER: MTA-025.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 732 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-989-299-5

Query Match 31.1%; Score 1334; DB 3; Length 732;
Best Local Similarity 42.6%; Pred. No. 6.5e-119; Indels 18; Gaps 7;
Matches 255; Conservative 112; Mismatches 213;

Qy 20 TIEQAKTFLDKFNHEDLPYQSSLASWNTNTITEENVQNNNAGDKWSAFLKEQSTL 79
Db 69 TDEAKADRFVEEDRTSQVWMEYAEANWNTNITTSKILKSTEVSHHTLYGTR 128
Qy 80 AQWYPLCEIQNLTVKLOLQALQONGSSVLSEDSKRLNTILNTMTSTYSGKVCNPDNPQ 139
Db 129 AKTFDVSNFQSSIKRIIKLQNLDRVLPPKELEVNQILLDMETTSLSNICVTNG-- 186
Qy 140 ECLLLEPGLEINMANSLDYNERLWAMESRSVGVKQLRPLYEYVVLKXEMARAHYEDY 199
Db 187 TCMLEPDLTNVMTSRKYEDLLWAMEGWEDKAGRAILOFPYKYVELINQAA 246
Qy 200 GDYWRGDYEVNGVDGYDSRQQLDEVEHTFEEIKPLYSHLHAYVRAKLMAVPS-YISP 258
Db 247 GDSWRSLYESDLE-----QDLKLYOELQPLYLNLHAYVRSRHRHYGSEYINL 296
Qy 259 IGCPLPAHLGDMGWFNLSYLVFPFGQKPNIDVTDAVVDQAWDAQRIFFEAEKEFFVS 318
Db 297 DGEIPALHGNWAGTWSNIYDLVVPFSPASMDTTEAMLKQGMTPRIFKEADNFTSL 356
Qy 319 GLENMTQGWENSMLETDGNVQKAVCHPTAWDLGKG-DFRILMCTKVTWDDLTAEHMG 377
Db 357 GLLPVPEPFNWSKMLEKFTDGRVVCCHASAWDFYNGKDFRIKQCTVWMDLVIAHENG 416
Qy 378 HIQYDMAYAAQFLLRNGANGSFHEAVEIMSLSAATPKHLKSLGLSPDQFQDNETEIN 437
Db 417 HIQYFMQYKDLFVTFREGANFGFHEAIGDINALSVSTPKHLYSLNLLSTE-OSGYEYDIN 475
Qy 438 FLLKQALTTVGLTPFTYMLEKRWNVFKGIPKQDQWKKWMEKREIVGVVFPVPHDET 497
Db 476 FLKMALDKIAFIPEFSYLDQWRVFDGSIKENYNOEWWSRLKYQGLCPVPRSQD 535
Qy 498 CDPASLHVSNDYSIRYVTRTYQFQFALCOAAGHGLKCDISNSTAGOKLPMN 557
Db 536 FDPGSRFHPANVPVIRYVFSFIQFQFALCOAAGHGLKCDISNSTAGOKLPMN 595
Qy 558 LRLKGEKPEKTLAENVGAKNNVRPLNYPELFTWLDKQNK--NSFVGM-STDWSP 612
Db 596 MKLGYSKFPEAKLITGQNNMSAMNYFKPLTEWLTENRRRHGHTLGLWPEYNWAP 653

RESULT 6
US-08-989-299-8
; Sequence 8, Application US/08989299
; Patent No. 6194556
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; CITY: Boston
; STATE: MA
```

```

; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,299
; FILING DATE: 11-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold E., Beth
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-025.01
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1312 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-989-299-8

Query Match 31.1%; Score 1334; DB 3; Length 1312;
Best Local Similarity 42.6%; Pred. No. 1.7e-118;
Matches 255; Conservative 112; Mismatches 213; Indels 18; Gaps 7;

QY 20 TIEQAKTFLDKFNEADLFYQSSLASWNYNTNITEENVQNNAGDKWSAFLEQSTL 79
DB 649 TDEAKADFVEIDYTAQVLNVEANWQYNTNITEGSKILLEKSTFVSHHTLYKGT 708
QY 80 AQMYPLEIQNLTVKLOLQALQONGSSVLSEDKSKRLNTILNTMTIYSTGKVCNPNPQ 139
DB 709 AKTFVSNFQNSIKRIIKLQNDRAVLPPKELEBYNQILLDMETTYSVANVCYTN 766
QY 140 ECLLEPGLNEIMANSLDYNERLWAWESWSEVGKQLRPLYEYVVLKNEMARAHYEDY 199
DB 767 TCMLEPDLTNMVAISRYKVEELLMAWKSWRDKVGRALPPFPKYVEFSNKIANGYTD 826
QY 200 GDYWRGDYEVNGVDYSGQLIEDVHTFEIKPLYEHLHAYVRAKLMAYPS-YISP 258
DB 827 GDSWRSLSYSDMLE-----QDLKLYOELQPLYNLHAYVRRSLHRYGSEYINL 876
QY 259 IGLPAHLGDMGWGFNTNLSLTVPGQKPNIDVTDAMVDQAWDAQRIKFAEKFFVSV 318
DB 877 DGPPIAHLGNNWQAQTSNIYDLVAPPSPAPNIDATEAMIKQGWTPRIFKEADNFTSL 936
QY 319 GLPNMTQGFWNSMLTDPGNVOKAVCHPTAWDLGK-DPRILMCTKVMTDDFLTAHHEMG 377
DB 937 GLLPVPPEFWNKSMLKPTDGRVVCVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHEMG 996
QY 378 HIQDMAYAAQFLLRNGANGFHEAVGEIMSLSAATPKHLKSLIGLLSPDQEDNETIN 437
DB 997 HIQYFMQYKDLVPTFREGANPGFHEAIGDLMALSVSTPKHLSLNLSTE-GSGYEYDIN 1055
QY 438 FLIKQALITVGLTPFTYMLKRWVNFKEIPKQDNWKNWEMKREIVGVVFPVPHDET 497
DB 1056 FLMKWALDKIATIPPSYILTDWRWRVFDGSIKENYQEWWSURLKYQGLCPVPRSQD 1115
QY 498 CDPASLPHYSNDYSIRYVTRTLVQFQFQALCOAAGHGLPKDCISNSTAGOKLFNM 557
DB 1116 FDPGSKFHPANVPVVRVVFVFIQFQFHEALCEAAGHTGFLHKDIIYOSKAGKLADA 1175
QY 558 LRLKGEPTLALENVGAKQNNVRPLNLYPELFTWLKQNK--NSFVGN--STWSP 612
DB 1176 MKLGYSKWPPEAMKLITQPNMSAMNNYFKPLTEWLVTEENRRHGETLGNPEYNWAP 1233

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RESULT 7

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US-08-989-299-9
; Sequence 9, Application US/08989299
; Patent No. 6194556
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Robinson, Keith E.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,299
; FILING DATE: 11-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold E., Beth
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-025.01
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1313 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-989-299-9

Query Match 30.5%; Score 1310; DB 3; Length 1313;
Best Local Similarity 42.0%; Pred. No. 3.5e-116;
Matches 251; Conservative 115; Mismatches 214; Indels 18; Gaps 7;

QY 20 TIEQAKTFLDKFNEADLFYQSSLASWNYNTNITEENVQNNAGDKWSAFLEQSTL 79
DB 650 TDEAKADFVEIDYTAQVLNVEANWQYNTNITEGSKILLEKSTFVSHHTLYKGT 709
QY 80 AQMYPLEIQNLTVKLOLQALQONGSSVLSEDKSKRLNTILNTMTIYSTGKVCNPNPQ 139
DB 710 AKTFVSNFQNSIKRIIKLQNDRAVLPPKELEBYNQILLDMETTYSVANVCYTN 767
QY 140 ECLLEPGLNEIMANSLDYNERLWAWESWSEVGKQLRPLYEYVVLKNEMARAHYEDY 199
DB 768 TCMLEPDLTNMVAISRYKVEELLMAWKSWRDKVGRALPPFPKYVDFSNKIAKNGYSDA 827
QY 200 GDYWRGDYEVNGVDYSGQLIEDVHTFEIKPLYEHLHAYVRAKLMAYPS-YISP 258
DB 828 GDSWRSLSYSDMLE-----QDLKLYOELQPLYNLHAYVRRSLHRYGSEYINL 877
QY 259 IGLPAHLGDMGWGFNTNLSLTVPGQKPNIDVTDAMVDQAWDAQRIKFAEKFFVSV 318
DB 878 DGPPIAHLGNNWQAQTSNIYDLVAPPSPAPNIDATEAMIKQGWTPRIFKEADNFTSL 937
QY 319 GLPNMTQGFWNSMLTDPGNVOKAVCHPTAWDLGK-DPRILMCTKVMTDDFLTAHHEMG 377
DB 938 GLLPVPPEFWNKSMLKPTDGRVVCVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHEMG 997
QY 378 HIQDMAYAAQFLLRNGANGFHEAVGEIMSLSAATPKHLKSLIGLLSPDQEDNETIN 437
DB 998 HIQYFMQYKDLVPTFREGANPGFHEAIGDLMALSVSTPKHLSLNLSSB-GSGYEYDIN 1056

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QY 438 FLLKQALITVGLTLPFTMLEKRWVVFKEIPEKQOMKMKWEMKREIVGVVPEVPHDET 497
Db 1057 FLMDWALDKAFIPESVLIDOWRVPDGSITKENYNGEWSLKKYQGLCPVPSRQGD 1116
QY 498 CDPSLHVSNDYSFTRYTRILYQFOFOALCOAKHGLPHKCDISNTEAGOKLFNM 557
Db 1117 PDPSKHFVPAVPIRYIFISFIQFOFHEACRAAGHTGLYKCDIYQSKAGKLLADA 1176
QY 558 LRLKSEPTWLTALENVVGAQNNVRPLNLYFPLFTWLKQNK--NSFVGW--STDKSP 612
Db 1177 MKLGYKQWPEAMKIITGQPNWSASAIMYFKPLTEWLVTEVRRRHGETGLGWPTWTTP 1234

RESULT 8
US-08-989-299-10
; Sequence 10, Application US/08989299
; Patent No. 6194556
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Robinson, Keith E.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
; AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,299
; FILING DATE: 11-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold E., Beth
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-025.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1310 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-989-299-10

Query Match 29.9%; Score 1283.5; DB 3; Length 1310;
Best Local Similarity 36.8%; Pred. No. 1.2e-113;
Matches 275; Conservative 135; Mismatches 262; Indels 75; Gaps 17;
QY 7 LLLSLVAVTAQSTII-----EQAKTFDKFNHEADLFYQSSLASNNYNTNI 54
Db 21 LLLLLRPPPAALTLDPGLPGDPADEAGARLFASSYNSSAEQVLPFRSTAASWADTNI 80
QY 55 TEENVONNAGDKWSAFLEKQSTLAQMYPLOEI-----ONLT---VKLQALQNGSS 106
Db 81 TAENARQEE-----EALLSQEFAEWGKAKELYDPVQWFTDPDRIIGAVRTLGPA 135
QY 107 VLSEDKSKRLMTLNTWTSTYTGKVCNPNFONFOECLELLEPGLEIMANSLDYNERLWAE 166
Db 136 NLPLAKRQOYNSLSNNSQIYSTGKVCFFNKTASCWSLDPDLNILLASSRSYAMLLFAWE 195
QY 167 SWRSVGRQLRPLYEEVWLKNEAMAHYEDYGRGDEYVNGVGDYDYSRQLJEDV 226

Db 196 GWHNAVGIPLKPLYQEBFTALSNEAYRQDGFSDTGAYWRSWYDSPTFE-----EDL 245
QY 227 EHTEREIPLYEHLHAYYRAKLNNAY--PSYISPIGCLPAHLGLDMWGRFTWNLXSLTVPF 285
Db 246 ERIYQLEPLYLNLHAYYRVLRVLRHRYGDRYINLRGIPAHLLGNWMAQSWESIYDMVVPF 305
QY 286 GQKPNIDVTAMDQMDAQRIKFAEKFPVSVGLPNWQGFWENSMLTDPGNVQKAVCH 345
Db 306 PKPKNLDVTWYQKGNWATHMFRVAEBEFTSLGLLPMPEFMAESMLEKPKDGDREVVCH 365
QY 346 PTAWDL--GKSGDPRILMCKVTMDDELTAHHEMGIHIOYDMAYAAQFPFLLENGANEGFHEAV 404
Db 366 ASADFYNKDFRIKQCTQVTMDOLSTVHHEMGIHIOYDMAYAAQFPFLLENGANEGFHEAV 424
QY 405 GEIMSLAATPKHLKSLIGLSDFDQEDNETEINFLKQALTIIVGLTLPFTMLEKRWVVF 464
Db 425 GDVLALSYSTPAHLKIGLLD--HYTNTESDIYLLKMALEKIAFLPGYLVQDQWGVF 483
QY 465 KGEIPKQOMKMKWEMKREIVGVVPEVPHDETCDPASLPHVSNDSYFIRYTRILYQFO 524
Db 484 SORTESSRYNFDWYLRKYQICPPVVRNETHFDAGAKFHIPSVTPYIRYFVSVLQFO 543
QY 525 FOEALCOAKHGLPHKCDISNTEAGOKLFNMLRLKSEPTWLTALENVVGAQNNVRPL 584
Db 544 FHQALCMEAGHQPLHQCDIYQSTRAGAKLRAVLQAGCSRPMQEVLDKMWASDALDAQPL 603
QY 585 LAYEPLFTWLKQNKNS--FVGW--STDWSPYADQSIKVRISLKSALG-----DKA 632
Db 604 LDYFQVTCWLOEQNERNGEVLGWPEYQWNPPLPNNYPEGIDLVIDEAESRFBVEYDRS 663
QY 633 YE--WND-----NEMYLFRSSVAYANRQYFLKVKQOMILFGEEDVRVANLAPRISFNPF 684
Db 664 FOAVMNEYAEANWYNTWITTEASKILLQKMOIANHTLYG-----NWARRFDVSNF 716
QY 685 VTAP-----KNVSD---IIPRTEVEK 702
Db 717 QNATSKRIIKKVKQDLQRAVLVPKLEEE 743

RESULT 9
US-08-989-299-6
; Sequence 6, Application US/08989299
; Patent No. 6194556
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Robinson, Keith E.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
; AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,299
; FILING DATE: 11-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold E., Beth
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-025.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 737 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-989-299-6

Query Match 29.9%; Score 1283; DB 3; Length 737;
Best Local Similarity 40.8%; Pred. No. 5.2e-114;
Matches 250; Conservative 112; Mismatches 213; Indels 38; Gaps 10;

QY 20 TIEQAKTLDKFNHEADLFVQSSLASWNTNITEE-----NVQNMN--AGDKW 69
DB 75 TDEAERFVEYDRSFQAVNVAEAWNTNITEASKILLQKMOIANHITYGNW 134
QY 70 SAPLEQOSTLAQWYPLQIQNLTKVLQLOALQONGSVLSDESKSLNTILMTNSTIY 129
DB 135 -----ARRFVSFQFQATSKRIKKVQDLQRAVLVPEKLEBYNQILDMETIYV 184
QY 130 GKVCNPDNPQECLELLEPGLNEIMANSLDYNERLWAMESRSEVQKQRLPYEYVVLXNE 189
DB 185 ANVCRVDG--SCLQLEPDLTNLMATSKYDELLWMTSMRDKVRAILPYEYVFTNK 242
QY 190 MABANHYEDYDYGVDYVNGVDYDYSRQQLIEDVEHTFEIKPLYEHLHAYVRAKLM 249
DB 243 AARLNGYVDAGSWSMYETPILE-----QDLERLFQELQPLYLNLHAYVGRALH 292
QY 250 NAY-PSYISPIGCLFAHLLGDMWRFTWNLVSLTVPEGQPNIDVTDAWVQDAQAQRI 308
DB 293 RHYGACHINLEGPFAHLLGNMWAQTNWNIYDLVAPPSASTNDATAMIKQGTPTRMF 352
QY 309 KEAEKEFFVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGK--DPRILMCTKVMD 367
DB 353 EADKXFFISGLLPVPEPFNKSMLKXPTDGRVVCCHASAWDFYNGKDFRIKQCTVANE 412
QY 368 DFLTAHHEMGIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSLGLSPD 427
DB 413 DLVVVHHEMGIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSLGLSPD 472
QY 428 FQEDNTEINFLKQALITVGLTPTMYLEKRWVFKGPIKQDQNMKRWKMEKREIVGV 487
DB 473 -GGYSHDINFLKQALITVGLTPTMYLEKRWVFKGPIKQDQNMKRWKMEKREIVGV 531
QY 488 VEPVPHDITYCDPASLPHVSNIDYSPRYTITLYQFQEQALQAAKHEGPHKCDISNS 547
DB 532 CPAPRSQGFDFGAKFHIPSSVPYRVFSFIQFQEQALQAAKHEGPHKCDISNS 591
QY 548 TEAGOKLFNKLRLGKSEPLTALENVYCAKMNVRPLLYFEPLFTWLKQDN--KNSFVG 605
DB 592 KEAGKRLADAMKLGYSKPEWEMKVIITQPNNSASAMNIFKPELDWLLTENGHRGEXKIG 651
QY 606 W-STDWSPYADOS 617
DB 652 WQYTTWTPNSARS 654

RESULT 10

US-08-989-299-11
Sequence 11, Application US/08989299
Patent No. 6194556
GENERAL INFORMATION:
APPLICANT: Accion, Susan L.
APPLICANT: Robinson, Keith E.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOGY
AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA

ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,299
FILING DATE: 11-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold E. Beth
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MIA-025.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-989-299-11

Query Match 25.4%; Score 1090; DB 3; Length 615;

Best Local Similarity 36.6%; Pred. No. 1.3e-95;
Matches 224; Conservative 122; Mismatches 244; Indels 22; Gaps 9;
QY 8 LLSLVAVTAAQSTIEQAKTFLDKFNHEADLFYQSSLASWNTNITEE NVQNMNAGD 67
DB 8 LLATLAVTAAQVKEEIQAKYLENLKELAKTNVTEAAWAGNSITDENKKNEISA 67
QY 68 KWSAPLEQOSTLAQWYPLQIQNLTKVLQLOALQONGSVLSDESKSLNTILMTNSTIY 127
DB 68 ELAKFMKEVASDITTKQWRSYQSEDLKQKQKALTKLGYAALPEDDYAELLDTLSAMESNF 127
QY 128 STGVKCPNDPQEC-LLLBPGLNEIMANSLDYNERLWAMESRSEVQKQRLPYEYVVL 186
DB 128 AKVVCYDKOSTCDLADPEIEEVISKRSRDEELAYRBYFDKAGTAVRSQERIVEL 187
QY 187 KNEMARANHYEDYDYGVDYVNGVDYDYSRQQLIEDVEHTFEIKPLYEHLHAYVRA 246
DB 188 NTKAALNNFTSGAEAWLDEYE-----DDTFEQQLEDI---FADIRPLYQQIHGVVF 237
QY 247 KIMNAY-PSYISPIGCLFAHLLGDMWRFTWNLVSLTVPEGQPNIDVTDAWVQDAQAQ 305
DB 238 RLKHYGDVAVSETGPIPMELLGNMWAQNSKADIVSFPFEKPLVDVSAEWKQAYTPL 297
QY 306 RIFKEAEKFFVSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAWDLGK--DPRILMCTKV 364
DB 298 KMFQMGDDFFTSNMLTKLPQDFWKSIIIEKPTDGRDLVCHASAWDFYLLIDVRIKQCTRV 357
QY 365 TMDDFLTAHHEMGIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSLGL 424
DB 358 TQDQLFTVHHEMGIQYFLQYQHPFVYRTGANPGFHEAVGVDLSVSTPKHLEKIGLL 417
QY 425 SPDFQEDNTEINFLKQALITVGLTPTMYLEKRWVFKGPIKQDQNMKRWKMEKREI 484
DB 418 K-DYVRDDEARINQLFLTALDKIVFLPFAFTMDKRWLSLFRGEYDKNWNCFAWKURDEY 476
QY 485 VQVVEPVPDITYCDPASLPHVSNIDYSPRYTITLYQFQEQALQAAKHEGPHKCDISNS 538
DB 477 SGIEPFPVVRSEKDFADAPAKYHISADVEYLRVLSVFIIFQFYKSACTKAGQYDNDVPEL 536
QY 539 LHKCDISNSTEAGOKLFNMLRGLKSEPLTALENVYCAKMNVRPLLYFEPLFTWLKQDN 598
DB 537 LNCDDIYGSARAGAAFNMLSMGSKXPDALFAFNGERIMSGRAIAPYFPEPLRWLEAE 596
QY 599 N--KNSFVGWST 608
DB 597 NIKNVHIGWTT 608


```
RESULT 11
US-09-440-325A-1
; Sequence 1, Application US/09440325A
; Patent No. 6280994
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: 98-79
; CURRENT APPLICATION NUMBER: US/09/440,325A
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(694)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-440-325A-1

Query Match      23.1%; Score 990; DB 3; Length 694;
Best Local Similarity 32.3%; Pred. No. 6.4e-86;
Matches 241; Conservative 121; Mismatches 258; Indels 126; Gaps 22;

QY 22 EQAKTFLDKFHEADLFYQSSLASNYNTNITEENVQNNAGDKWSAPLKEQSTLAQ 81
DB 53 ETETKIFLQYDQGTGEVLNKFMEATWNTVITNTRKQENNMKDMER-SQFMIFYGTQAH 111
QY 82 MYPLQEIQNTVKKLQALQOQNGSSVLSSEKSKRLNTILNTMTSTIYTGVCNPDNPQEC 141
DB 112 LFKVTFKPDVNGMLSKLONIDKAALSDEIRREYNELLAXLEMTYSMAQVCLNEG- 169
QY 142 LLEPGLINEIMANSLDYNERLMAWESRSEVKQRLPYEEYVVLKEMARAH-YEDYG 200
DB 170 LSLSEL-EYMATSRDEKELLMAWQGDVGRQICITFEHYVELSKAAQLNGVXKDMG 228
QY 201 DYNRGDYEVNGVDGYDSRGQIEDVHTFBEIKPLHYHLHAYVRAKLMNAY-PSYISPI 259
DB 229 ALWHSKYESDTLE-----QDLERLFQELRPLYNPHYVRRALHRYGPELIDLR 278
QY 260 GCLPAHLIGD-MWGRFWNTLYSLTVPFGOKENIDVTDAWQDAQORI-FKEAEKFFVS 317
DB 279 GPIPAHLGENTLAQSWNILDVPLFKIPEDVTIKMKVQHWKPEKLMLEAEETFTY 338
QY 318 VG--LPNMTQGFWNSMLTDPGNVQKAVCHPTANDLKG-GDPRILMCTKVTMDDFLTAHH 374
DB 339 LGLALPAPPSPFWKLMLEMRPTDGREVECHISAWNIFYQDDDFRIKKCAEVTEDPLSIFH 398
QY 375 EMGHIQYDMAAQAQPFLLRNGANEGFHEAVGEIMSLAATPKHLKSLIGLLSPQFQEDNET 434
DB 399 EMGHFQYFLQYKNLSIIFRTGANPAFEAAGSVITLSASSHKHLNIGLLS--LLED--- 453
QY 435 EINLLKQALTIQVTLPTFTYMLKEMWVKEGEIKDQWKKQWEMER-EIVGVVEVPH 493
DB 454 EVNFMHIALEKIAFIIFGIMDLFRKVDFTGIMDIYNQEWNNRLKTKQGLCPAIPH 513
QY 494 DETYCDPASLPHVSNDSYFI-RYYTTLTQFOQOALCOAAHEGPHKDKISNSTBAQ 552
DB 514 SEEDDFDPAKHFAGVPIRRYFLSLVLFQFQFHETLCKASGMGMLHQCDDIYNSKIAG 573
QY 553 KLFNMLRLKSEPMFTLALENVGAKNNVRPLINPEPLFTMLKQNKNSFVGWSTDWSP 612
DB 574 LL--ALKLGSSKPWPEVLKMLTGESEVSNVFTYFKPLLTLN----- 614
QY 613 YADQSIKVRISLKGALGKAYENDNEMYLFRSSVAYANRQYFLKVNQMILFQEDVRV 672
DB 615 -----VTEHAARGE----- 623
QY 673 ANLKPRISNFNFVTPAKXVSDIIPRTEVEKAIIRMSRINDAFRLNDNSLEFLGIQPTLG 732

Db 624 ---TPGVPLQFY--PPYET-----PMSSTEK-----DTRKVTFLSLKL--- 656
QY 733 PPNQPPVSIW-LIVFGVVMGVIVGCI 757
DB 657 DNQAKFGYVILLALGFVMSLVVLGL 682

RESULT 12
US-09-846-996A-1
; Sequence 1, Application US/09846996A
; Patent No. 6524635
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Zacl: A Human Metalloenzyme
; FILE REFERENCE: 98-79D1
; CURRENT APPLICATION NUMBER: US/09/846,996A
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US 09/440,325
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 60/109,783
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (152)...(152)
; OTHER INFORMATION: Xaa is any amino acid.
; NAME/KEY: VARIANT
; LOCATION: (224)...(224)
; OTHER INFORMATION: Xaa is any amino acid.
US-09-846-996A-1

Query Match      23.1%; Score 990; DB 4; Length 694;
Best Local Similarity 32.3%; Pred. No. 6.4e-86;
Matches 241; Conservative 121; Mismatches 258; Indels 126; Gaps 22;

QY 22 EQAKTFLDKFHEADLFYQSSLASNYNTNITEENVQNNAGDKWSAPLKEQSTLAQ 81
DB 53 ETETKIFLQYDQGTGEVLNKFMEATWNTVITNTRKQENNMKDMER-SQFMIFYGTQAH 111
QY 82 MYPLQEIQNTVKKLQALQOQNGSSVLSSEKSKRLNTILNTMTSTIYTGVCNPDNPQEC 141
DB 112 LFKVTFKPDVNGMLSKLONIDKAALSDEIRREYNELLAXLEMTYSMAQVCLNEG- 169
QY 142 LLEPGLINEIMANSLDYNERLMAWESRSEVKQRLPYEEYVVLKEMARAH-YEDYG 200
DB 170 LSLSEL-EYMATSRDEKELLMAWQGDVGRQICITFEHYVELSKAAQLNGVXKDMG 228
QY 201 DYNRGDYEVNGVDGYDSRGQIEDVHTFBEIKPLHYHLHAYVRAKLMNAY-PSYISPI 259
DB 229 ALWHSKYESDTLE-----QDLERLFQELRPLYNPHYVRRALHRYGPELIDLR 278
QY 260 GCLPAHLIGD-MWGRFWNTLYSLTVPFGOKENIDVTDAWQDAQORI-FKEAEKFFVS 317
DB 279 GPIPAHLGENTLAQSWNILDVPLFKIPEDVTIKMKVQHWKPEKLMLEAEETFTY 338
QY 318 VG--LPNMTQGFWNSMLTDPGNVQKAVCHPTANDLKG-GDPRILMCTKVTMDDFLTAHH 374
DB 339 LGLALPAPPSPFWKLMLEMRPTDGREVECHISAWNIFYQDDDFRIKKCAEVTEDPLSIFH 398
QY 375 EMGHIQYDMAAQAQPFLLRNGANEGFHEAVGEIMSLAATPKHLKSLIGLLSPQFQEDNET 434
DB 399 EMGHFQYFLQYKNLSIIFRTGANPAFEAAGSVITLSASSHKHLNIGLLS--LLED--- 453
QY 435 EINLLKQALTIQVTLPTFTYMLKEMWVKEGEIKDQWKKQWEMER-EIVGVVEVPH 493
DB 454 EVNFMHIALEKIAFIIFGIMDLFRKVDFTGIMDIYNQEWNNRLKTKQGLCPAIPH 513
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QY 494 DETYCDPASLHNDYSEFL-RYVTRTLQFOFEOALCOAAHREGPLHKCDISKSTRAGQ 552
DB 514 SEEDFDPAKHPFAGVPYIRHFLSLVJQFHEILCKASGHMGLHCDIYNSKIAK 573
QY 553 KLFNMLRGKSEPTWLALENVGAAMNVRPLNYPFLFTWLDKONKNSFVGMSTWSP 612
DB 574 LL--ALKLGSCKPMPFVLKMLTGSEVSTNVFVTFKPLLTWL----- 614
QY 613 VADQSKVIRISLKGALGPKAYEMNDNEMYLFRSSVAYAMRQVFLKVKVQMLFGSEEDVRV 672
DB 615 -----VIEHARGE----- 623
QY 673 ANLKPRISFNFTAPKNSVDIIPRTEVEKALRMSRINDAFRLNDSLEPLGIQPTLG 732
DB 624 ---TGVPLQFY--PPHYT-----PMSSTK-----DTCVTFLSKL----- 656
QY 733 PNPQPPVSIW-LIVFGVVMGVIVGI 757
DB 657 DPNQAKFGYVLLALGFVMSLVVLGL 682

RESULT 13

US-08-989-299-12
Sequence 12, Application US/08989299

Patent No. 6194556

GENERAL INFORMATION:

APPLICANT: Acton, Susan L.

APPLICANT: Robinson, Keith E.

TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG

TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESS: FOLEY, HOAG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/989,299

FILING DATE: 11-DEC-1997

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Atwood E., Beth

REGISTRATION NUMBER: 35,430

REFERENCE/DOCKET NUMBER: MIA-025.01

TELEPHONE: 617-832-1000

TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 907 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-989-299-12

Query Match

Best Local Similarity 15.0%; Score 642.5; DB 3; Length 907;

Matches 172; Conservative 136; Mismatches 289; Indels 41; Gaps 19;

QY 2 SSSWLLSLVAVTAQAQSTIEQAKTFLDPFNHEDBLFVQSSIASWNTNTNTEENVQN 61

DB 160 SSNYKTNLQAPGSIKD--BEKRLSWLAGYEAKVLFREVALSVGMRYFNDSPLSLKA 217

QY 62 MNNAGDKWSAFLEKQSTLAQMPYEQIQLNTVQLQALQOQNGSSVLSKSKRLNTILN 121

DB 218 LDEAVNLTVPRSTSMQAKQPDMAVSVDKVMRQLGVVSPGMSALAPSPFADYSOQA 277
QY 122 TMSIYIYTGKVCNPDNPQECGLLEPGLNIMANSLDYNERLMAWESWESEVKGQLRPLYE 181
DB 278 ALNRDSKSDICDNDVPPCALQKIDMSIFRNEKDSRLQHLWVSYVTAIAXS-KPSYN 336
QY 182 EYVWLQEMARAHYEDYDYNRGDYEVNG-VGVYDYSRGQIEDVEHTFBEIKPLYEHL 240
DB 337 NIITISNEGAKLNGFANGAMRSADFMSKVEKAEF---DLNKQIDKIYSTIQPFYQLL 393
QY 241 HAYVRALKMAY--PSYISPIGCLPAHLGLDMGRENWNLVSLTPFGOKNIDVTDAMV 298
DB 394 HAYMERQLAGIYSPVGLSKDGPAPHLFGSLDGGDSAHYEQTKPFREES--ETPEAML 451
QY 299 D-----QAWDAQRIPEAKKFFVSGLPNMTQGFWNSMLTDPGNVQKAVCHP-TANDL-G 352
DB 452 SAFTQNTYTKKMFVTAIRYFKSAGFPHLPKSTWTSISIFARVWS-KDWICHFAALDMRA 510
QY 353 KGDFRILMCTKVTMDDELTAHHEMGIQYDMAAQAQPFLLRNGANEGFHEAVEIMSLSA 412
DB 511 PNFVRVKAQGLGEPDEQAHSLLVQTYQYLYKQOSLLFREQASPVITDAIANAFHLS 570
QY 413 ATPKHLKISIGLLSPDFQDNETS-INFLKQALTIIVGTLPTMYMLEKRWVFKGEIKPD 471
DB 571 TNPVLYSOKLVPSEHLDIKDSVINKLYKESLESFTKLPTFIADNWRVYELFDGTVERN 630
QY 472 OMKKWEMKREIVGVVPEVPHDRTYCDPASLPH---VSNIDYSFIRYTRTL----YQFQF 525
DB 631 KINDRWBEIRNKYGVRSQPQYNTSNLD--ALHNSVSQVHS---PATRILISYVYLKFOI 685
QY 526 QEALCQAA---KHEGPHLHKCDISNSTEAGOKLFNMLRLGKSEFPWTLALENVVGAKNMVR 582
DB 686 LKALCQRELFWLSEG---CILSEDTT--EKLRETKLGSITLWLKALEMISGKGLDAQ 739
QY 583 PLLNYFPELFTWLKDNK--NSFVGRSTOWSPYADQSI 618
DB 740 PLEIYEPLNLWLRNTEIDQVVVVGWDGEGTPTTVEEI 777

RESULT 14

US-09-996-243-387

Sequence 387, Application US/09996243

Patent No. 6478825

GENERAL INFORMATION:

APPLICANT: Ashtenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Guiney, Austin L.

APPLICANT: Kijavini, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tamas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: P2730P1C13

CURRENT APPLICATION NUMBER: US/09/996,243

CURRENT FILING DATE: 2001-11-14

PRIOR	FILING DATE: 1998-06-12	
PRIOR	APPLICATION NUMBER: 60/089440	
PRIOR	FILING DATE: 1998-06-16	
PRIOR	APPLICATION NUMBER: 60/089512	
PRIOR	FILING DATE: 1998-06-16	
PRIOR	APPLICATION NUMBER: 60/089514	
PRIOR	FILING DATE: 1998-06-16	
PRIOR	APPLICATION NUMBER: 60/089532	
PRIOR	FILING DATE: 1998-06-17	
PRIOR	APPLICATION NUMBER: 60/089538	
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 PRIOR FILING DATE: 1998-06-26
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 PRIOR FILING DATE: 1998-07-02
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 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091626
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 8.8%; Score 376; DB 4; Length 212;
 Best Local Similarity 47.9%; Pred. No. 8e-28;
 Matches 75; Conservative 32; Mismatches 48; Indels 6; Gaps 3;

Qy 612 PVADQIKVIRISLKGALGDKAYENDNEMYLFRSSVAYAMQVFLKVNQMLFGEEDVR 671
 Db 19 PGANAFKVRSLRTALGADKAYADTNEEYLFKAMVAFNR---KVPRESAT-BISHVL 73
 Qy 672 VAMKPRISFNFTAPKNVSDIIFRTEVEKAIKMSRSINDAFRLNDNSLEFLGIQPTL 731
 Db 74 LCNVTORVSFWPVTDPK-NHTLPAVEVQSARIMKMKRINNAPFLNDOTLEFLKIPSTL 132
 Qy 732 GPNQPPVSMILVGV 776
 Db 133 APMPDPSVIMLIGVIFCIIIVAILLILSLGWORRRKNKEPS 177

RESULT 15

US-09-107-532A-6507
 Sequence 6507, Application US/09107532A
 Patent No. 6583275
 GENERAL INFORMATION:
 APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 NUMBER OF SEQUENCES: 7310
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 City: Waltham
 State: Massachusetts
 COUNTRY: USA
 ZIP: 02354
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD-ROM ISO9660
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 FILING DATE: 30-Jun-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 FILING DATE: 14 May 1998
 APPLICATION NUMBER: 60/051571
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ariniello, Pamela Deneke
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 6507:

SEQUENCE CHARACTERISTICS:

LENGTH: 615 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...615

SEQUENCE DESCRIPTION: SEQ ID NO: 6507:

US-09-107-532A-6507

Query Match 3.1%; Score 131; DB 4; Length 615;

Best Local Similarity 20.1%; Pred. No. 0.0016;

Matches 127; Conservative 87; Mismatches 227; Indels 190; Gaps 31;

Qy 3 SSSWLLLSLVATAAOSTIEBOAKTFDKFNHBAEDLFYSSSLASWYNTNTNTEENVQM 62
 Db 20 SLNWNLDSPFGSGSHSDALNQMKOLEQDQNE-----YYHRTVKNSPSS---DNAEQL 69
 Qy 63 NNAGDKMSAPLKEQSTL-----AQMYPLEQIEON 90
 Db 70 N-----AILQIQETITNGTQSSYITALLSANVDSDAKVLGKLYAMLPRLOSAET 122
 Qy 91 L-----TVKLQALQONGSSVLSEDKSKRLNTI---LNTM 123
 Db 123 VLSKPAEISDNDNQMLSQSSFEIAPRLNEIRDSQSLSEAEINIITLSLDGINAW 162
 Qy 124 STLYST--GKVCNP--DNQECLELLEPG--LNEIMAN--SLDYNERLA--AWESWSEVGLQ 176
 Db 183 SSIHYDIIVASISIPPEQGVVLSAGAFNKGMDPKVRETLFAWE-----BAWKEK 238
 Qy 177 RPLVEYVVLKNEMARANYEDYDYNRGDYVNGVDYDYSRGQIEDVEHTFEIKPL 236
 Db 239 APLFTDTL-----NELDGR---LSDYELHGVV---DFLQ-----KEL 270
 Qy 237 YEHLYAVRAKLNNAYPSYISPIGCLPAHLGDMWGRFTNLYSLVTFPGQKFNIDVDA 296
 Db 271 -----EYNRLK-----KETLSVMMDTIQKNKQPLVNYLTRKANLFGKEK 309
 Qy 297 MVDQANDAOEI-----PKAEKFPV-----SVGLPNNMTQGFWNSML---TDPG 337
 Db 310 MEWQDQDAPIILGLDKKTFDFDEAAAFIENWKFSPKMAKTAQSAFESKSWIEADRP 369
 Qy 338 NVQKAVCHPTANDLGKDPFRILMCTKVTDMDFLTAHEMGHIOYDMAYAAQPFLLNGAN 397
 Db 370 KRFGGYC--TELPETK--ESRIFMTYSNVNEVATLAHELGHAFHSSTMDLPSL-----N 421
 Qy 398 EGFHEAVGEIMSLSA-----ATPKHLSIGLLSPDFQEDNETEINFL---LQALTIIVG 448
 Db 422 REYAMNVAETASTFAELIVADATLKVAKT-----KEEKINLLDTKLQNALAMP 470
 Qy 449 TLPEPTVMLE--KVRMVFKGEIPKQMKMKWEMKREIVGVVPEVPHDEYCDPASLFHVS 507
 Db 471 NIHSRIFENRVEARQGLVSEDKI--EMMVYEAQKE--GYQGLATYTHYFYFAAKLHFFI 528
 Qy 508 NDYSFIRY-YTTLVQF 537
 Db 529 DNVFFYNFPYT---FGYLFSLGIYAYANQKG 556

Search completed: February 19, 2004, 19:52:14

Job time : 24 secs